

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 23:01:30 ; Search time 4143 Seconds
(without alignments)
11410.342 Million cell updates/sec

Title: US-09-665-308D-11
Perfect score: 2259
Sequence: 1 acaactctccactcattc.....ttaaaaaaaaaaaaaaa 2259

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	603	26.7	1574	6	AX339396	AX339396 Sequence
2	379.8	16.8	1788	6	A85060	A85060 Sequence 4
3	377.2	16.7	1951	8	ATCD1	X83369 A.thaliana
4	328.4	14.5	1162	8	AMA250396	AJ250396 Antlrthln
5	152.6	6.8	1679	6	A85058	A85058 Sequence 2
6	152.6	6.8	1679	6	NTA011893	AJ011893 Nicotiana
7	143.8	6.4	1487	8	AB015222	AB015222 Nicotiana
8	137.2	6.1	1140	8	AMA250397	AJ250397 Antlrthln
9	134.6	6.0	1460	8	LEAJ2589	AJ002589 Lycopers1
10	134.4	5.9	1414	6	A85061	A85061 Sequence 5
11	131.6	5.8	1650	8	ATCD2	X83370 A.thaliana
12	129.8	5.7	1861	8	MSCYCPROT	X88864 M.sativa MR
13	127.2	5.6	1699	8	CRCYCD	Y10162 C.rubrum MR
14	123.4	5.5	1449	8	LEAJ2590	AJ002590 Lycopers1
15	123	5.4	1632	8	ATCD3	X83371 A.thaliana
16	122	5.4	1370	8	AY062645	AY062645 Arabidops
17	120.8	5.3	1431	6	A85059	A85059 Sequence 3
18	120.8	5.3	1431	8	NTA011894	AJ011894 Nicotiana
19	120.4	5.3	1532	8	LES245415	AJ245415 Lycopers1
20	118.8	5.3	1518	8	LEAJ2588	AJ002588 Lycopers1
21	118.6	5.3	1628	8	AB008188	AB008188 Pisum sat
22	116.8	5.2	1284	6	A85057	A85057 Sequence 1
23	116.8	5.2	1284	8	NTA011892	AJ011892 Nicotiana
24	116	5.1	1086	8	AY063729	AY063729 Arabidops
25	116	5.1	1351	8	AY052665	AY052665 Arabidops
26	112.2	5.0	1846	6	A85077	A85077 Sequence 21
27	107.4	4.8	1214	8	CRU011776	AJ011776 Chenopodi
28	101.6	4.5	114505	8	F20P5	AC002062 Sequence
29	101.4	4.5	1451	8	AMA250398	AJ250398 Antlrthln
30	97.8	4.3	927	6	A96985	A96985 Sequence 1
31	97.8	4.3	1179	8	ATH131636	AJ131636 Arabidops
32	85	3.8	4553	8	MSA132929	AJ132929 Medicago
33	83.4	3.7	3054	8	MSA132930	AJ132930 Medicago
34	82.2	3.6	119856	2	AP004005	AP004005 Oryza sat
35	78.2	3.5	94091	8	ATF28A23	AL021961 Arabidops
36	78.2	3.5	192861	8	ATCHRIV80	AL161584 Arabidops
37	78.2	3.5	195921	8	ATCHRIV81	AL161585 Arabidops
38	75.8	3.4	6657	8	AF208693	AF208693 Arabidops
39	74.2	3.3	15290	8	AB025614	AB025614 Arabidops
40	70.8	3.1	108158	8	ATF3A4	AL132978 Arabidops
41	66	2.9	7218	6	I66494	I66494 Sequence 14
42	56.4	2.5	9504	6	AX323793	AX323793 Sequence
43	54.4	2.4	1141	6	AX083744	AX083744 Sequence
44	53.6	2.4	5525	6	AX281352	AX281352 Sequence
45	53.6	2.4	5525	6	AX347365	AX347365 Sequence

ALIGNMENTS

RESULT 1
AX339396
LOCUS AX339396 1574 bp DNA linear PAT 10-JAN-2002
DEFINITION Sequence 1 from Patent WO0196579.
ACCESSION AX339396
VERSION AX339396.1 GI:18135592

KEYWORDS
SOURCE barrel medic.
ORGANISM Medicago truncatula

REFERENCE
AUTHORS Miskolczi,P., Pettko-Szantner,A., Horvath,G., Dudits,D., Fehér,A.
and Gyorgyey,J.
TITLE A novel plant cyclin
JOURNAL Patent: WO 0196579-A 1 20-DEC-2001;
CropDesign N.V. (BE)
FEATURES
source location/Qualifiers
1. .1574
/organism="Medicago truncatula"
/db_xref="taxon:3880"

Db 704 TATCGGCTTCTTTCGCACAAATCGATCCATCTGGAATGTATACGGGTTCTCTTATCTC 763
QY 787 CAGGGCAACAGAAATCATCTGATCTATATATCCAGAGGCTAGCTTCTTCTTACTGGCC 846
Db 764 AAGGGCAACACAAATATCTCTCAATATATCAAGAACTAGTTACTTGAATTTGGCC 823
QY 847 TTCATGCAATGCTGCTGACGACCTACTCAGCTGACGTAATGAATTCCTAATGGTCTGT 906
Db 824 ATCATGTATGCTGCTGACCAATACCTTGTGACGACGATGATCTTCTAAATCTCACT 883
QY 907 GGTAAAGCCGAAATGCTGATCATGTGCGAGGACCTAAGAAAGAAAGTAATAGG 966
Db 884 TATCAATGCTGATCATGCTGATCATGTGTGATGGCTTAGCAAGAGAGATCACAA 943
QY 967 GTGCTACCACTTGATCAA 985
Db 944 ATGTTACAGACTTGACAA 962

RESULT 3
ATCD1
LOCUS ATCD1 1951 bp mRNA linear PLN 25-MAR-1998
DEFINITION A.thaliana mRNA for cyclin delta-1.
ACCESSION X83369
VERSION X83369.1 GI:2995129
KEYWORDS cyclin; cyclin delta-1.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
TITLE A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
JOURNAL Plant Cell 7 (1), 85-103 (1995)

JOURNAL MEDLINE
REFERENCE 95210930
2 (bases 1 to 1951)
AUTHORS Murray,J.A.H.
TITLE Direct Submission
JOURNAL Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK

REMARK
REFERENCE 3 (bases 1 to 1951)
AUTHORS Murray,J.A.H.
TITLE Direct Submission
JOURNAL Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK

COMMENT
FEATURES On Mar 28, 1998 this sequence version replaced gi:603504.
location/Qualifiers
1. 1951

/organism="Arabidopsis thaliana"
/variety="ecotype Landsberg erecta"
/db_xref="taxon:3702"
/tissue_type="whole seedlings"
/clone_lib="pFl61"
/dev_stage="seedlings, stage 2 leaves"
104. 1111
/codon_start=1
/product="cyclin delta-1"
/protein_id="CAA58285.1"
/db_xref="GI:2995130"
/db_xref="SWISS-PROT:P42751"
/translation="MRSYRFSDDLHMSVFSNDMDLFCGEGDSGYFSGESTVDFSSSEV
DSWPGDSIACFLIEDERHFVPGHDYLSRQTRSLDASAREDSVANILKYQAYYNFQPLT
AYLAVNYMDRFLYARLPETSGWPMQLAVACLSLAKMREILVPSLDFOVAGVKYL
FEAKTIKRMELLYLVLDWRLRSVTPDFISFAKIDPGETGLGFFISHATEIILSN
IKEASFLEYWPSIIAAAILCVANELPSLVNPHSPETWCDGISKEKIVRCYRLM
KAMAIENNRLNTPKVIKLRVSVRASSILTRPSDESSPCRRKRLSGYSWVGDETST
N"

misc_feature 134. 283

/note="pest motif, potential"
167. 181
misc_feature /note="LXCXE motif"
344. 661
misc_feature /note="cyclin box"
860. 898
misc_feature /note="pest motif, potential"
1019. 1051
BASE COUNT 535 a 327 c 451 g 638 t
ORIGIN
Query Match 16.7%; Score 377.2; DB 8; Length 1951;
Best local similarity 68.7%; Pred. No. 5.6e-81;
Matches 552; Conservative 0; Mismatches 243; Indels 9; Gaps 2;
QY 297 CAGAGATGTTATTCGATCGCGAGCTTCATCGACGACGAGCGCACTTCGTCGGGAT 356
Db 300 ATGATTATCTCTAGATTTCAAACTCGATCTCGATGCTCCGCTAGAGAATTCGG 359
Db 240 CATGGCCTGGTATCTATCGCTTGTATTGAAAGACGAGCGCTCATCTCCTGAC 299
QY 357 TCGAGTACCTGTCGCGGTTCCATCTCGCTCCCTGAGCGCCAGCCAGAGAATCAG 416
Db 300 ATGATTATCTCTAGATTTCAAACTCGATCTCGATGCTCCGCTAGAGAATTCGG 359
QY 417 TTGATGATTCGACAGGTACACGCGCTATGCTTTCAGCCTTTGACGGCGTACCTG 476
Db 360 TCGCATGATTCGACAGGTACACGCGCTATGCTTTCAGCCTTTGACGGCGTACCTG 419
QY 477 CCGTCACTATATGATTCGGTTTGGATTCGCGGTTGCGGGAACAATGGTGGC 536
Db 420 CCGTATATATGATTCGGTTTGGATTCGCGGTTGCGGGAACAATGGTGGC 479
QY 537 CTCTGCAACTGTATCTGTTGATGCTGCTTTGGCAGCAAGATGGAAGAACCTCTG 596
Db 480 CAATGCAACTTTAGCAGTGGCATGCTGCTTTAGCTGCAAAAGATGGAAGAACCTCTG 539
QY 597 TTCATCTCTCTGACCTTCAGATAGAGAGCCAAAGTACATATTTGAGCCGAGAACAA 656
Db 540 TTCCTTCTCTTTGATTTTCAGTTTCAGTTGACGAGTGAAGTATTTATGAAACAACCTA 599
QY 657 TTCGTAGATGAGACTTCTGTTCTCGGTTCTAGATTGAGGCTAAGATCAGTAACAC 716
Db 600 TAAAGAAGATGAACTCTTCTGTTCTAAGTGTGTTAGATTGAGACTAAGATCGTTACAC 659
QY 717 CACTTGTCTCTCGCTTCTTCTGCGTGAAGATAGATTCAACTGGAATTTTATCCGGT 776
Db 660 CGTTGATTTCAATACCTTCTTCTGCTTACAGATCGATCCCTTCGGGTACTTCTCGGGT 719
QY 777 TCCTATTTCCAGGCAACAGAAATCATCTGATCTAATATCCAGAGGCTAGCTTCTTG 836
Db 720 TCTTATCTCCCATGCTACAGAGATTATCTCTCAACATAAAGAAAGCAAGCTTCTTG 779
QY 837 CTTACTGGCCTTCATGCAATGCTGCTGACGACCTACCTCAGCTAATGAATTCCTA 896
Db 780 AGTACTGGCATGAGTATAGCTGACGCGGATTTCTGTGTAGCGAAGAGTTACCTT 839
QY 897 ATTGCTC-----TGTGTTAAGCCCGAAAGTCTGAGTCATGTTGCGAGGAGTAAGAA 950
Db 840 CTCTATCTCTGTTGCTCAATCCCCACGAGAGCCCTGAGACTTGTGTGACGAGATTGAGCA 899
QY 951 AAGAAAAGTAATAGGCTGTACAGTTCATGATCAAGAGCTTGTGATTAACAATAACCAAC 1010
Db 900 AAGAGAAGATAGTGAATGCTATAGACTGATGAAGAGGATGGCCATCAGAAATAACCGGT 959
QY 1011 GGAAGTCCCTTACTAAAGTGTTCGCCGACCTGCGAGTAA---CAACTCGGACCCGAA 1067
Db 960 TAAATACACCAAAAGTATGACAAAGCTTCAGTGAAGGCAATCATCGAGCTTAA 1019
QY 1068 TGAGGTCAAGTACTGATCATCAT 1091
Db 1020 CAAGGCCAAGTATGATCTCTCTT 1043

RESULT 4

LOCUS AMA250396 1162 bp mRNA linear PLN 15-NOV-1999
DEFINITION Antirrhinum majus mRNA for cyclin D1 (cyclin gene).
ACCESSION AJ250396
VERSION AJ250396.1 GI:6448479
KEYWORDS cyclin gene; cyclin D1.
SOURCE snapdragon.
ORGANISM Antirrhinum majus

REFERENCE 1 (bases 1 to 1162)
AUTHORS Gaudin, V., Lunness, P., Fobert, P., Towers, M., Riou-Khamlich, C., Murray, J., Coen, E. and Doonan, J.H.
TITLE The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated by the cycloidea gene

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1162)
AUTHORS Doonan, J.H.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM

FEATURES
source location/Qualifiers

1. .1162
/organism="Antirrhinum majus"
/db_xref="taxon:4151"
/dev_stage="flower spike"
139. .1131
/gene="cyclin D1"
139. .1131
/gene="cyclin D1"
/codon_start=1
/product="cyclin D1"
/protein_id="CAB61221.1"
/db_xref="GI:6448480"

BASE COUNT 333 a 268 c 246 g 315 t
ORIGIN
/translation="MSLSCDCEFSDLCEGDSNIIIFSGGDDLPETSDVESIPTDVD
ESIALGLEDERDLAGVNSSSSNOSVDSSTRSTAMILKVQRYGQPLTAYLAVSYF
DRFLNAHLPLKNGWPMQLSLVACLSLAKMESLVPSLDLQVGNFIPEPNRQ
MELLVRLVLDWRLRSISPCYLSFALKIDPTGTYTGFILSRKELILSTVQETSLIE
YRPSCIAATMLSSANDLPKFSFITAQHAEMCDGLHKDNIASCILIOGVESNNRPK
KQPKVLPLQRLVMTTRASLASSESSSSPSYKRRKLNNSSRADDDKESSDYGV"

Query Match 14.5%; Score 328.4; DB 8; Length 1162;
Best Local Similarity 64.6%; Pred. No. 4.1e-69;
Matches 548; Conservative 0; Mismatches 276; Indels 24; Gaps 3;

QY 382 TCCTCCCTGAGCGCCAGCAAGCAAGATCAGTTGATGATTCCTCAAGTACACGC 441
DB 336 TCAATCGGTGATTTCTTCTACTAGAACAGATCTACCGCATGATCCTCAAGTGCACG 395
QY 442 GTACTATGCGCTTTCAGCGCTTTCAGCGCTACCTCGCGTCAACTATATGATCGGTTTTT 501
DB 396 TTATTTACGGTTTTCAGCGCTTTCAGCGCTATCTCGCGTTCAGCTTCTGATCGTTTTCT 455
QY 502 GGATTCGCGCGGTGCGCGAACAATGGGTGCGCTTCGCAACTTGATCTGTTCGATG 561
DB 456 AAACGCCCATCACTGCGCGAAGTTGAATGGGTGCGCAATGCAACTATGTCCGTTGCGTG 515
QY 562 CTGTCTTTGGCAGCAAGATGGAAGAACCTCTGTTCATCTCTCTTGACCTTCAGAT 621
DB 516 CTGTCTATTAAGCTGCTAAGATGAGGAATCTCTGTCTCTCTCTTTTGATCTTCAGGT 575
QY 622 AGAAGTGCCCAAGTACATATTTGAGCCGAGAACAAATTCGATGAGATGAGCTACTTGTCT 681
DB 576 GGAAGGACAACTTATTTTGAACCAAGAAATATCCAAAGATGAGAGCTTCTGTGCT 635
QY 682 CGGTCTTAGATTGAGAGCTAAGATCAGTACACCACTTGTCTCTCGCTTCTCTTTC 741
DB 636 TAGGGTTTAGATTGAGAGCTTGGGTCAATATCTCCATTTGTATCTCAGCTTTTTCGC 695

QY 742 GTCAAAAGTAGATTCAACTGGAACCTTTATCCGGTTCCTTATTTCCAGGCAACAGAAAT 801
DB 696 ACTCAAAATCGACCCCAACTGGAACCTTATACAGGTTTCTGACGCAAGGCTAAAGAAAT 755
QY 802 CATCGTATCTAATATCCAAAGAGGCTAGCTTCTTCTGCTTACTGGCTTCATGATGCTGC 861
DB 756 TATCTCTCAACCGTTCAAGAGACCAGTTGATGAGTATAGGCATCATGATGCTGC 815
QY 862 TGCAGCCATCTACTGACGCTGACGCTAATGAATTCCTAATTTGGTCTGTGTTAAGCCCGAAA 921
DB 816 TGCAACAATGCTTTTCAATCGGCAATGATCTGCCAAAATTTCTTTCATCATCTGCTCAACA 875
QY 922 TGCTGAGTCAATGCTGCGAGGAGCTAAGAAAAGAAAAGTAATAGGGTCTACCACTGAT 981
DB 876 TGCTGAGGCAATGCTGATGATGACTTCAACAAGATAATATTTGCTAGTTGCATCAAACTGAT 935
QY 982 GCAAGAGCTTGTGATTAACAATAACCAAGGAACTCCCTTACTAAAAGTGTGCGCA 1041
DB 936 TCAAGAGTGAATCAACAATAGGCCAAAAAGCAGCCC-----AAGGTTTACCACA 989
QY 1042 GCTCGAGTAACTCGGACCCGAATGAGGTCAAGTACTGTATCATCTCATGATC 1101
DB 990 GCTCCGAGTCACTGCTCGGCGAGTTTGCGCTCGAGT-----GAATCGTC 1034
QY 1102 CTCTCAACCTCTCTCTCTGTGTGTAAGAGAGGAAATTAATAA---CCGTTGTG 1158
DB 1035 ATCATCTACCTCGCTCTCGCCCTCTTATTAAGAGGAAATTAATAGCTCTCGGC 1094
QY 1159 GGTAGATGACAAAGAACTCCGAGTGAAGAGAAAAGCAACAATAATTAAGAGAGG 1218
DB 1095 GGATGATGACAAAGAGAGCTCTGATTTATGGGGTCTAAATTAAGGATTAAGGATTAAGG 1154
QY 1219 AAGAAAAA 1226
DB 1155 AAAAAAAA 1162

RESULT 5

LOCUS A85058 1679 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 2 from Patent WO9842851.
ACCESSION A85058
VERSION A85058.1 GI:6733799
KEYWORDS
SOURCE common tobacco.
ORGANISM Nicotiana tabacum

REFERENCE 1 (bases 1 to 1679)
AUTHORS Murray, J.A.
TITLE PLANTS WITH MODIFIED GROWTH
JOURNAL Patent: WO 9842851-A 2 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
FEATURES
source location/Qualifiers

BASE COUNT 537 a 281 c 293 g 568 t
ORIGIN
/organism="Nicotiana tabacum"
/db_xref="taxon:4097"

Query Match 6.8%; Score 152.6; DB 6; Length 1679;
Best Local Similarity 52.2%; Pred. No. 3e-26;
Matches 338; Conservative 0; Mismatches 309; Indels 0; Gaps 0;

QY 372 GGTTCATCTCGCTCCCTGAGCGCAAGCCAGAGAAATCAGTTGATGATTCCTCA 431
DB 455 GTTTTCAAGATGACTCTTACTCTGTTCGCCCGTGTGATTCGTGAATGATTTTAA 514
QY 432 AGGTACAGCGCTATAGGCTTTCAGCGCTTGAAGCGGTACCTGCGCTCAACTATATGG 491
DB 515 AAGTGAATGTTTATAGGTTTCTCTGCTTGAAGTCCGTTTGAAGCATAATTTACTTGG 574

RESULT 7	LOCUS	DEFINITION	AB015222	1487 bp	mRNA	linear	PLN 02-APR-1999
AB015222	AB015222	Nicotiana tabacum Ntcyd3-1 mRNA, complete cds.					
ACCESSION	AB015222						
VERSION	AB015222.1	GI:4586800					
KEYWORDS	Ntcyd3-1.						
SOURCE	Nicotiana tabacum						
ORGANISM	Nicotiana tabacum cell_line:BY-2	CDNA to mRNA.					
REFERENCE	1	(bases 1 to 1487)					
AUTHORS	Sekine,M.						
TITLE	Cell cycle regulated gene						
JOURNAL	Published Only in Database (1999)	In press					
REFERENCE	2	(bases 1 to 1487)					
AUTHORS	Sekine,M.						
TITLE	Direct Submission						
JOURNAL	Submitted (03-JUN-1998)	Masami Sekine, Nara Institute of Science and Technology, Graduate School of Biological Sciences; Takayama 8916-5, Ikoma, Nara 630-0101, Japan					
COMMENT	(E-mail:sekine@nara.ais.t-nara.ac.jp, tel:+81-743-72-5462, Fax:+81-743-72-5469)						
FEATURES	Sequence updated (19-Aug-1998).						
SOURCE	Location/Qualifiers						
	1..1487						
	/organism="Nicotiana tabacum"						
	/db_xref="taxon:4097"						
	/cell_line="BY-2"						
	136..1242						
	/gene="Ntcyd3-1"						
	136..1242						
	/gene="Ntcyd3-1"						
	/codon_start=1						
	/protein_id="BAA76478.1"						
	/db_xref="GI:4586801"						
	/translation="MGIOHNEHNDQTSFLLDALYCEEERWETIEDEIEKEATLP LPPLLEQDLFWEDDELLSFTKEKETISNFEITIKDPLCLSRKEAVKWLKVNAY GFSTFALIAINFDRLSSLFHFKDKWMIQVAVTCLSLAKVEEVOPLLDFOV EDAKYFEAKTIQRMELLVLSLKWNRANVPLSFVDHIIRRLGLKSHIWEFLKQCE RILLVIADCRFLSYMPSVLATATMLHYHVEPCNADYQNLLEVLNLSKEKVNDC YELITEVSINYSISHKRKYESPINSPSAVIDTFYSSSENSNESWDLOTSSIPSTYSPRD QFLPLFKSRVQEQQMRLLTSLSRVFDVAVGSPR"						
	1487						
	/note="18 a nucleotides"						
BASE COUNT	462 a	257 c	287 g	481 t			
ORIGIN							
Query Match	6.4%;	Score 143.8;	DB 8;	Length 1487;			
Best Local Similarity	52.2%;	Pred. No. 4.2e-24;					
Matches 319;	Conservative 0;	Mismatches 292;	Indels 0;	Gaps 0;			
408	AAGAATCAGTTGGATGATCTTCAAGGTACACGCGTACTATGGCTTTAGCCCTTTGACGG	467					
401	AAGAAAGCTGTGAANGAGATCTTAAAGTAAATGCTCATATGGAATTCACACATTCAC	460					
468	CGTACCTCGCCGTCACATATATGATCGGTTTTTGGATCTCGCCGGTGGCCGGAACAA	527					
461	CTATTCCTTGCTATTAATTAATCTTTGATAGGTTCTTTCAAGCTTCATTTTCAGAAAGATA	520					
528	ATGGGTGGCCTCTGCAACTGTATCTGTTGCATGCTTGCTTTGGCAGCAAAAGATGAAG	587					
521	AGCCTTGATGATTCACACTGTAGCTGTACTGTCTTCTTTGGCTGCTAAAGTTGAAG	580					
588	AACCTCTGTTCATCTCTTTGGACCTTCAGATAGAAGTCCCAAGTACATATTTGAGC	647					
581	AAACTCAAGTTCCTCTCTTTTGGACTTCACAGTGAGAGATCAAAATATGTGTTGAGG	640					
648	CGAGACAATTCGTAGATGAGACTACTGTCTCGGTGCTTGAATTGAGGCTAAGAT	707					
641	CCAAAACTATTCAAGAAATGAGCTTTTGGTATGTGCTCTTTAAAGTGAGAGATGAATC	700					

QY	708	CAGTAACACCACTTTGGCTTCCTCGCTTCTCTTGGCGTGCAAAAGTAGATTCAACTGCAACTTT	767
Db	701	CTGTAAACCCCACTTTCATTGTGTGATCATATATAAGAACTTGGGCTAAAGAGCCATA	760
QY	768	TTATCCGGTTCCTTATTTTCCAGGGCAACAGAAATCATCTATCTAATATCCAAAGGCTA	827
Db	761	TACACTGGGAATTTCTCAAGCAGTGTGAGAGAATTCCTCTTTTGGTCATAGCTGATTTGA	820
QY	828	GCTTTCCTGCTTACTGGCCCTCATGCACTTGTCTGTGCAACCATCTCACTGCAGCTAATG	887
Db	821	GATTCCTTAAGTTATATAGCCTCTCTGTATTGGCTACTGCACTATGCTTCACGTTATTATC	880
QY	888	AAATTCCTAATTGTCGTGTGGTTAAGCCCGAAAAATGCTGAGTCATGTGCGAGGACTAA	947
Db	881	AAGTTGAGCCTTGTATATGCTGCTGACTACCAAAATCAACTTCTTGAGGTTCTCAACATTA	940
QY	948	GAAAAGAAAAAGTATATAGGCTGTACCAAGTTGATGCAAGAGCTTGTGATTAAACATAACC	1007
Db	941	GCAAGGAGGAAGGTGAATGATTTGCTATGAACCTTATAACAGAGGTGCTTACAACCTTATTTT	1000
QY	1008	AACGGAAACTC 1018	
Db	1001	CACACAAGCGC 1011	

RESULT	8
LOCUS	AMA250397
DEFINITION	AMA250397 1140 bp mRNA linear PLN 15-NOV-1999
ACCESSION	Antirrhinum majus partial mRNA for cyclin D3a (cycD3a gene).
VERSION	AJ250397
KEYWORDS	AJ250397.1 GI:6448481
SOURCE	cycD3a gene; cyclin D3a.
ORGANISM	snappdragon.
REFERENCE	Antirrhinum majus
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum. 1 (bases 1 to 1140)
TITLE	Gaudin,V., Lunness,P., Fobert,P., Towers,M., Riou-Khamlichl,C., Murray,J., Coen,E. and Doonan,J.H. The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated by the cycloidea gene unpublished
JOURNAL	2 (bases 1 to 1140)
REFERENCE	Doonan,J.H.
AUTHORS	Direct Submission
TITLE	Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM
JOURNAL	location/Qualifiers
FEATURES	1..1140
source	/organism="Antirrhinum majus"
	/db_xref="taxon:4151"
	/dev_stage="flower spike"
	110..1139
	/gene="cycD3a"
	110..>1139
	/gene="cycD3a"
	/codon_start=1
	/product="cyclin D3a"
	/protein_id="CAB61222.1"
CDS	/db_xref="GI:6448482"
gene	/translation="MYQONSPSLCFDALYCEEQNMDNGELINDCFIEQEPEFSDLK HDLTCGVDDDDDKKEISSLCKEQEYELYRVLEDNPSLAKARDEAVEMFKVIGYYS FSALTAVLAIVYLDRFLCTFQFGQDKPMWQLAAVACLSLAKAVEETOVPLLLDLOVE ESKYVFESKTIFORMELLVLSTLKWKMPVTPISFLEYIARIALKSHCKEFILNRCEC LLLSLTDCRFMCHLPALATATMLYITSSLEPCIGVEYQDQLINIGINKDKVEEC KLIOEVATSVHFQSGNKRRKFGSLPYSPKVVDISFCSDSWPLDSTASVSSSPEHLISK KIKTONPDH"
BASE COUNT	332 a 223 c 237 g 348 t
ORIGIN	

[illegible]

REFERENCE	1 (bases 1 to 1650)
AUTHORS	Soni, R., Carmichael, J.P., Shah, Z.H. and Murray, J.A.
TITLE	A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif
JOURNAL	Plant Cell 7 (1), 85-103 (1995)
MEDLINE	95210930
REFERENCE	2 (bases 1 to 1650)
AUTHORS	Murray, J.A.H.
TITLE	Direct Submission
JOURNAL	Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK	Revised by [3]
REFERENCE	3 (bases 1 to 1650)
AUTHORS	Murray, J.A.H.
TITLE	Direct Submission
JOURNAL	Submitted (07-JUN-1996) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK	revised by [4]
REFERENCE	4 (bases 1 to 1650)
AUTHORS	Murray, J.A.H.
TITLE	Direct Submission
JOURNAL	Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
COMMENT	On Mar 28, 1998 this sequence version replaced gi:1402895.
FEATURES	Location/Qualifiers
source	1. .1650

CDS	195..1280	/codon_start=1	/product="cyclin delta-2"	/protein_id="CA58286.1"	/db_xref="GI:2995132"	/db_xref="SWISS-PROT:P42752"	/translation="MAENLACGETSESWIINDDDDDINYGGEFTNEIDYNHQLEAKDDNFGNGSIPTMGSSSSLSSEDRIKEMLVREIEFCPGTDYVKRLLSGDDLVSRLQALDNLKVCAYHFEGLHCLISLMSNYLDRFLSYELPKDKWAQOLLAVSCSLASKMEETDVPHIVDLQVEDPKFVFEAKTIKRMELLVTTLNWRQALTPESFIDYVDKISGHVSENLIRSSRFILNTTKAIEFLDFRPSLEIAAASVSISGETECIDEKALSLIYVKQERVKRCILNMRSLTGEENVRGTSLSQEQARVAVRVAPSPGVLEATCLSYRSEERTVESCSTNSQSSPDNNNNNNNSNKRKRKKQ"	207..221	/note="LXCXE motif"	318..392	/note="pest motif, potential"	480..798	/note="cyclin box"	915..992	/note="pest motif, potential"	1118..1259	/note="pest motif, potential"	BASE COUNT	528 a	293 c	346 g	483 t	ORIGIN
Query Match	5.8%;	Score 131.6;	DB 8;	Length 1650;																			
Best Local Similarity	54.0%;	Pred. No. 4e-21;																					
Matches 294;	Conservative	0;	Mismatches 244;	Indels	6;	Gaps	1;																
QY	335	GAGCGCAACTTCGTCGCGGATTCGAGTACCTGTCGGCGTTCCAACTCGCTCCCTGGAC	394	111	1	11	11	11	11	1	11	11	11	11	11	11	11						
Db	414	GAGATTGAGTTTGGCCCTGGAAGTATATGTTAAGAGATTGCTTCTGCGATTGGAT	473	111	1	11	11	11	11	1	11	11	11	11	11	11	11						
QY	395	GCCACGCCAGAGAAGATCAGTTGATGATTTCTCAAGGTACACGCGTACTATGGCTTT	454	1	11	11	11	11	11	11	11	11	11	11	11	11	11						
Db	474	TTGTCTGTTCCGAACCAAGCTCTTGATTGGATTCTTAAGGTTTGTCCTCATTTACCATTTT	533	1	11	11	11	11	11	11	11	11	11	11	11	11	11						

QY	455	CAGCCTTGCACGGCCGTAACCTCGCCGTCACACTATATGGATCGGTTTGGATTCTCGCCGG	514
Db	534	GGACATCTGTGCATATGCCCTATCCATGAACCTACTTGGATCGGTTCTTAACATCCATATGAA	593
QY	515	TTGCCGGAACAATAATGGGTGGCCCTCTGCACACTGTGATCTGTGCATGCTGTCTTTGGCA	574
Db	594	TTGCCGAAGAAGACAAGATTGGGCTGCTCAGTTACTAGCTGTGCTTGTCTTATCATTTAGCA	653
QY	575	GCAAGATGGAGAACCTCTGTTCATCTCTCTTGGACCTTCAGATAGANGTGCCAAG	634
Db	654	TCCAAAATGGAGAAGAACTGATGTGCTCACAATTTGATTACAGGTGGAAGATCCCAAG	713
QY	635	TACATATTTGAGCCGAGACAATTCGTAGATGAGAGCTACTGTCTCGGTCTTAGAT	694
Db	714	TTTGTTTTGGGCCCAACAATAAAAAAGATGAGAGCTTTGGTGTGCACCACCTTGAAT	773
QY	695	TGAGAGCTAAGATCAGTAAACACCACTTGTCTCTCGCTTCTTGGCGTCAAGTAGAT	754
Db	774	TGGAGATTGCAAGCTCTTAACCTCATTCTCTCATTTGAATTTCTGTTGACAAGAT----	829
QY	755	TCAACTGGAACCTTTATCCGGTTCCTTATTTCCAGGGCAACAAGAAATCATCTGATATTAAT	814
Db	830	--CAGTGGTCACGTTGCGAGAAATTTGATCTATAGATCGTCAAGATTTCATGTTAAACACC	887
QY	815	ATCCAGAAGGCTAGCTTCTTGTCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATCTC	874
Db	888	ACCAAGAAGCAATTTGAATTTTAACTTCAGGCCCTTCTGAGATACCTGCACGCTGCTGCAGTG	947
QY	875	ACTG 878	
Db	948	TCTG 951	

RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
MSCYCPROT	1861 bp	mRNA	linear	PLN 25-JUL-1996			
MSCYCPROT	M.sativa mRNA for cyclin protein.						
X88864	X88864.1	GI:1150931					
	cyclin; cymc4 gene.						
	Medicago sativa.						
	Medicago sativa						
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.						
	1 (bases 1 to 1861)						
	Dahl, M., Mesiklene, I., Bogre, L., Ha, D.T., Svoboda, I., Hubmann, R., Hirt, H. and Heberle-Bors, E.						
	The D-type alfalfa cyclin gene cymc4 complements G1 cyclin-deficient yeast and is induced in the G1 phase of the cell cycle						
JOURNAL	Plant Cell 7 (11), 1847-1857 (1995)						
MEDLINE	96093424						
REFERENCE	2 (bases 1 to 1861)						
AUTHORS	Hirt, H.						
TITLE	Direct Submission						
JOURNAL	Submitted (20-JUN-1995) H. Hirt, Inst. of Microbiology & Genetics, Univ. of Vienna, Dr. Bohrergasse 9, 1030 Vienna, AUSTRIA						
FEATURES	Location/Qualifiers						
source	1. 1861						
	/organism="Medicago sativa"						
	/db_xref="taxon:3879"						
gene	243. 1403						
	/gene="cymc4"						
	243. 1403						
	/gene="cymc4"						
	/codon_start=1						
	/product="cyclin"						
	/protein_id="CAA61334.1"						
	/db_xref="GI:1150932"						
	/db_xref="SPTREMBL:Q40338"						
CDS							

```

/translation="MAIHNNHNNHQQLOOHTSSLFDALYCDDEEKWEDDECEVYVDEG
AQSDVTTNTNYDILDSTSLPLLEQNTLENEDELNLFSEKITQOEITYEDKNVIN
FDSLQPRREAVEVEMLKVNANHGCSFALYAVNYLDRLFLSFHQEKPMQIQLVAV
TCISLAKVEETQVPLLDLOVDQVDTKYVEAKTIQRMELLISTLTKMKMPVTHSFL
DHIIIRGLCKNLNLHWEFLRRCENLLSYLDSRFVGCVPVSLATATMLHAVIDQIEQSD
DNGVDYKQNLNVLKISKEKVEDCYNALIDHTNANNYGHKRKYEIIPGSSGVIDAVE
SSDGSNDSTWVGASSYSTSEPVFKTKKQGNMNLSPINRYIVGILATATSP"

```

Query Match	5.78;	Score 129.8;	DB 8;	Length 1861;
Best Local Similarity	55.1%;	Pred. No. 1.1e-20;		
Matches 254;	Conservative 0;	Mismatches 207;	Indels 0;	Gaps 0;
QY 410	GAATCAGTTGGATGGATTCCTCAAGGCTACACGCGGTACTATGGCTTTACAGCCTTTGACGGCG			469
Db 576	GAAGCTGTGATGATGGATGCTTAAAGTCAATGCTCATATATGGTTTCTCTGCTCTCACCTGCA			635
QY 470	TACCTCGCCGTCACCTATATGATCGGTTTGGATTCTCGCGCGTTGCCGGAACAAT			529
Db 636	ACACTTGTCTTAACTATCTTGATAGGTTTCTTTAAGCTTCCATTTCCAAAAAGAGAAA			695
QY 530	GGGTGGCCCTGCAACCTTGATCTGTGTCATGCTTGTTCGGCAGCAAAAGATGGAAGAA			589
Db 696	CCATGGATGATTCAGCCTGTGCTCTTACTTGCATCTCTTAACTGCTAAAGTTGAAGAA			755
QY 590	CCTCTTGTCCATCTCTTTGACCTTCAGATAGGAAGGTGCCAAGTACATATTTGAGCCG			649
Db 756	ACTCAAGTTCCTCTCTCTTAACTTCAAGTCAAGATGCAAGATCTAAATATGTGTTGAGCA			815
QY 650	AGAACAATTGCTAGAGATGAGCTACTTGTCTCGGTGCTTGTAGATGAGAGGCTAAGATCA			709
Db 816	AAGACTATTCAGAGAATGAGACTATGATTCTGTCAACACCTGAATGGAAGATGCATCCA			875
QY 710	GTACACACCACCTTGTCTCCCTCTTCTTTGGCGTCAAAAGTAGATTCACCTGGAACCTTTT			769
Db 876	GTGACACACACACTCTTTCTTAGATCACAATTAAGAAGGCTTGAATGAAACTAATCTT			935
QY 770	ATCCGGTCTCTATTTCCAGGGCAACAGAATCATCTGATCTAATATCCAAGAGGCTAGC			829
Db 936	CATTGGGAGTTCCTTAGCGCGCTGTGAGAATCTTCTTCTATCTGTACTTTTAGATTCACAGA			995
QY 830	TTTCTTGCTTACTGGCCTTCATGCATTCCTGTGCTGCAGCCAT			870
Db 996	TTTGTGTGCTGTCTCTCTGTGTGTGGCCCACTGCTACAAT			1036

RESULT 13				
CRCYCD				
LOCUS	CRCYCD	1699 bp	mRNA	linear
DEFINITION	C.rubrum mRNA for cyclin-D like protein.			
ACCESSION	Y10162			
VERSION	Y10162.1	GI:1770189		
KEYWORDS	cyclD gene; cyclin-D like protein.			
SOURCE	red goosefoot.			
ORGANISM	Chenopodium rubrum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.			
REFERENCE	1 (bases 1 to 1699)			
AUTHORS	Renz, A.			
TITLE	Direct Submission			
JOURNAL	Submitted (18-DEC-1996) A. Renz, Lehrstuhl fuer Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr. 30, 95447 Bayreuth, FRG			
REFERENCE	2 (bases 1 to 1699)			
AUTHORS	Renz, A., Fountain, M. and Beck, E.			
TITLE	Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic cell suspension culture of Chenopodium rubrum L			
JOURNAL	Plant Physiol. In press			
FEATURES	Location/Qualifiers			
source	1. .1699			
	/organism="Chenopodium rubrum"			

Db	636	GGAAGATGAATCCAGTAACCCCATTTTCATTTCTTGATTTTATACTAGAGACTTGGAT	695
QY	756	CAACTGGAACCTTTTATCCGGGTTCCTTATTTCCAGGGGCAAGAAATCATCGTATCTAATA	815
Db	696	TGAAGCACGTGCTTATCTTTGGAAATTTCTGAGGAGATGTGAGAAAGTGTCTTTTACACAA	755
QY	816	TCCAGAGGCTAGCTTTTCTTGCTTACTGGCCCTTCATGCAATGTGCTGTCAGCCATACTCA	875
Db	756	TTACTGATGATAGATTCATTTGTTGTTACCTTCCCTCTGCAATGGCATCTGCCACAATGTTGC	815
QY	876	CTGCAGCTAATGAATTCCTAATTTGGTCTGTGTTAAGCCCGAAATGCTGAGTCATGTT	935
Db	816	ATGTTCTTGATAGGCTTAAGCCTTGCAATTGGAGAAAGTACCAAGATCACTTTTGGGCA	875
QY	936	GCGAGGACTAAGAAAAAGAAAGTAATAGGGTGCTACCACTTGATGCAAGAGCTTGTGA	995
Db	876	TTCTTGGAAATTGTCAAGAGAGAGGTGGAAGGATGTTACAGGCTAATTACAAGAGTGGCTT	935
QY	996	TTAACATAAC	1006
Db	936	GCAACATTGAC	946

```

DLILQLPVDNRICLQIQIQSSKKRKSHDSSSLNSPSCVIDANPFNSDESSNDSWSASS
CNPPTSSSSPQQQPPPLKKMRGAENEKKRPILHLPMAlVATP"

misc_feature      329. 343
                   /note="lxCxE motif"
misc_feature      347. 472
                   /note="pest motif, potential"
misc_feature      521. 838
                   /note="cyclin box"
misc_feature      1169. 1393
                   /note="pest motif, potential"

BASE COUNT      478 a      369 c      317 g      468 t
ORIGIN

Query Match      5.4%; Score 123; DB 8; Length 1632;
Best Local Similarity 50.4%; Pred. No. 5e-19;
Matches 300; Conservative 0; Mismatches 295; Indels 0; Gaps 0;

OY      396 CCAACGCCAGAGAAGATCATGTGGATGGATTCTCAAGCTACACGGCTACTATGGCTTTC 455
      111 1 11 1111 11111111 1111111 11 1111 11111111
Db      516 CCACGATCGAAAAGAAGCTGTGGTGGATCTGAGAGTCACACGCTCATTTATGGCTTCT 575

```

LOCUS	ATCD3	1632 bp	mRNA	linear	PLN 25-MAR-1998
DEFINITION	A.thaliana mRNA for cyclin delta-3.				
ACCESSION	X83371				
VERSION	X83371.1 GI:2995133				
KEYWORDS	cyclin; cyclin delta-3.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
AUTHORS	1 (bases 1 to 1632)				
TITLE	Soni, R., Carmichael, J.P., Shah, Z.H. and Murray, J.A.				
REFERENCE	A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif				
JOURNAL	Plant Cell 7 (1), 85-103 (1995)				
MEDLINE	95210930				
REFERENCE	2 (bases 1 to 1632)				
AUTHORS	Murray, J.A.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK				
REMARK	revised by [3]				
REFERENCE	3 (bases 1 to 1632)				
AUTHORS	Murray, J.A.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK				
COMMENT	On Mar 28, 1998 this sequence version replaced gi:603508.				
FEATURES	Location/Qualifiers				
source	1. .1632				
	/organism="Arabidopsis thaliana"				
	/variety="ecotype Landsberg erecta"				
	/db_xref="taxon:3702"				
	/tissue_type="whole seedlings"				
	/clone_id="pFL61"				
	/dev_stage="seedling, stage 2 leaves"				
	266. .1396				

```

Db      576  CTACTTTAGCAGCTGTTTATGCCATACTTATCTCGATTAGTTCATCTGTAGCTACAGCT 635
QY      516  TGCCGGAAACAATGGGTGGCCCTCTGCAACTGTGATCTGTGCATGCTTGTCTTGGCAG 575
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      636  TACAGAGAGACAAACCATGGATGGCTTCAGCTCGTTTCGGCGGTGCTCTCATTAAGCTG 695
QY      576  CAAGATGGAAGAACCTCTTGTTCATCTCTCTTGAGACCTTCAGATAGAAGGTGCCAAGT 635
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      696  CTAAAGTCGAAGAAACCCAGTCCCTCTTCTTAGACTTTCAAGTGGAGAGACAAGT 755
QY      636  ACATATTTGAGCCGAGACAATTCGTAGGATGGAGCTACTTCCTCCGGTGTCTTAGATT 695
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      756  ATGTGTTTGAAGCAAAAACCATACAGAGAATGGAGCTACTGATTTCTGTCTACTCTCGAGT 815
QY      696  GGAGGCTAAGATCAGTAACACCACTTGTCTCTCGCTTCTTGTGCGTGCAAGTAGATT 755
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      816  GGAAGATGCATCTCATTTACTCCAAATTCGTTGTAGACCACATTAATCAGGAGATTGGGAC 875
QY      756  CAACTGGAACCTTTATCCGGTTCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATA 815
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      876  TTAGAACAATGCTCAGCTGGGATTTCCCTCAACAATAATGCCACCGTCTCCTCTGTAA 935
QY      816  TCCAAGAGGCTAGCTTTCCTTGCCTTACTGGCCCTTCATGCATTCCTGCTGCAGCCATACTCA 875
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      936  TCTCCGATTCAGATTTGTCCGGGTACCTCCCATCAGTAGTTCGCCGACCTACCATGATGC 995
QY      876  CTGCAGCTAATGAATTCCTAATGTGCTGTGGTTAAGCCCGAAATGCTGAGTCATGCT 935
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      996  GAAATTATAGAGCAAGTTGATCCCTTGAACCCCTCTTCATACCAACTAATCTCCTCGGTG 1055
QY      936  GCGAGGGACTAAGAAAAAGAAAAAGTAATAGGGTGTACCAAGTTGATGCAAGAGCT 990
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      1056  TCCTTACTTAACCAAGAAAAAGTGAAGAACTGCTACGATCTAATCTCCCACT 1110

```

Search completed: October 26, 2002, 01:34:54
Job time : 4150 secs

Search completed: October 26, 2002, 01:34:54
Job time : 4150 secs

translation="MAIRKEESREBQNSFLDALYCEEKWDDEGEVEEENSLSISS
/translating="MAIRKEESREBQNSFLDALYCEEKWDDEGEVEEENSLSISS
SSSPFVIAQDLEWEDDEDLYLFSKEEEQSCIDDDYLISTDRKEAVGMILRVNAHC
ESTLAVALATITLYDKFICSYSLGRDKPMLQLVSACSLAAKVEETQVPLLDNCH
ETKYVEAKTIOREMLLISLTLEWKMHLITPISFVDHILRLGLKNNAMHDFLNCHEH
LLSVISDSRFVGYLPSVAATAATMMRIIEQVDPDFPLSYQTNLLGVNLTKKAYCVCV

GenCore version 5.1.3
 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 22:39:44 ; Search time 366 Seconds
 (without alignments)
 10597.021 Million cell updates/sec

Title: US-09-665-308D-11
 Perfect score: 2259
 Sequence: 1 acactctccactcatc.....ttaaaaaaaaaaaaaaaaaa 2259

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_032802:*
 1: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1980.DAT:*
 2: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT:*
 3: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1982.DAT:*
 4: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1983.DAT:*
 5: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1984.DAT:*
 6: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1985.DAT:*
 7: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1986.DAT:*
 8: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1987.DAT:*
 9: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1988.DAT:*
 10: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1989.DAT:*
 11: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1990.DAT:*
 12: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1991.DAT:*
 13: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1992.DAT:*
 14: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1993.DAT:*
 15: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1994.DAT:*
 16: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1995.DAT:*
 17: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1996.DAT:*
 18: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1997.DAT:*
 19: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT:*
 20: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:*
 21: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT:*
 22: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
 23: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
 24: /SIDS1/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2259	100.0	2259	20	AAZ19958	Soybean cyclin del
2	689.6	30.5	1994	20	AAZ19959	Soybean cyclin del
3	388.4	17.2	1337	21	AAC42423	Arabidopsis thalia
4	379.8	16.8	1788	19	AAV33887	H. tuberosus thalia
5	152.6	6.8	1679	19	AAV33885	N. tabacum CYCD3;1
6	134.4	5.9	1414	19	AAV33888	H. tuberosus CYCD3;
7	122	5.4	1311	21	AAC40202	Arabidopsis thalia
8	120.8	5.3	1431	19	AAV33886	N. tabacum CYCD3;2
9	116.8	5.2	1284	19	AAV33884	N. tabacum CYCD2;1

10	116.2	5.1	1173	21	AAZ94583	Maize cyclin D zmc
11	116	5.1	1356	21	AAC51463	Arabidopsis thalia
12	116	5.1	1358	21	AAC33723	Arabidopsis thalia
13	112.2	5.0	1846	19	AAV33889	Maize cycD2 gene.
14	112.2	5.0	1861	21	AAZ94581	Maize cyclin D zmc
15	110.6	4.9	1077	21	AAZ94582	Maize cyclin D zmc
16	103.2	4.6	1932	20	AAZ19961	Corn cyclin delta-
17	99.4	4.4	1287	21	AAC48940	Arabidopsis thalia
18	99.4	4.4	1290	21	AAC39981	Arabidopsis thalia
19	97.8	4.3	927	20	AAZ36897	Mitogenic cyclin C
20	87	3.9	1007	20	AAZ19956	Corn cyclin delta-
21	83.8	3.7	1734	21	AAZ94584	Arabidopsis thalia
22	59.6	2.6	1122	21	AAC50081	Arabidopsis thalia
23	59.6	2.6	1721	21	AAC50083	Arabidopsis thalia
24	55.8	2.5	1223	21	AAC34244	Rice cyclin delta-
25	54.8	2.4	510	20	AAZ19957	Wheat cyclin delta
26	54	2.4	790	20	AAZ19963	Human metastasis a
27	53.6	2.4	5525	24	ABL34463	Human metastasis a
28	53.2	2.4	1732	21	AAC38832	Arabidopsis thalia
29	51.8	2.3	17721	24	ABL33729	Human immune syste
30	50.6	2.2	6076	24	ABL32364	Human immune syste
31	50.6	2.2	6076	24	ABL34480	Human immune syste
32	50.2	2.2	5919	24	ABL32388	Human immune syste
33	50.2	2.2	5919	24	AAZ61106	Human gene regulat
34	49	2.2	7849	24	AAD23229	Chemically treated
35	48.6	2.2	9731	24	ABL32990	Human immune syste
36	48	2.1	73334	24	ABL34125	Human immune syste
37	47	2.1	5268	24	ABL32876	Human immune syste
38	47	2.1	6161	24	AAZ61200	Human gene regulat
39	47	2.1	15881	24	ABL32260	Human immune syste
40	47	2.1	15881	24	AAZ61069	Human gene regulat
41	47	2.1	18817	24	ABL34495	Human metastasis a
42	46	2.0	16287	24	ABL32673	Human immune syste
43	45.8	2.0	6227	24	ABL34499	Human immune syste
44	45.8	2.0	10006	24	ABL32037	Human immune syste
45	45.8	2.0	10710	24	ABL32893	Human immune syste

ALIGNMENTS

RESULT 1
 AAZ19958
 ID AAZ19958 standard; cDNA; 2259 BP.

AC AAZ19958;

DT 21-DEC-1999 (first entry)

DE Soybean cyclin delta-1 cDNA.

KW Cyclin delta-1; soybean; cell cycle; cell division;
 transgenic plant; herbicide; plant breeding; ss.

OS Glycine max.

FH Key Location/Qualifiers
 FT CDS 167..1186

FT /*tag= a

PN WO9948486-A2.

PD 30-SEP-1999.

PF 19-MAR-1999; 99WO-US06047.

PR 23-MAR-1998; 98US-0078948.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Caloon RE, Klein TM, Odell JT, Orozco EM;

DR WPI; 1999-591036/50.

DR P-PSDB; AAY31894.

XX New isolated plant cyclin genes, used to develop products for use as
PT herbicides and for developing plant breeding programs -
XX
XX
PS Claim 7; Page 51-52; 68pp; English.

CC This nucleotide sequence represents a contig assembled from the
CC cDNA inserts in clones sahic.pk003.17 and sri.pk0001.95 encoding
CC the entire soybean cyclin delta-1 protein (see AAY31894). These
CC clones were respectively isolated from soybean sprayed with
CC Authority (TM) herbicide and soybean root cDNA libraries. The
CC invention relates to isolated nucleic acid fragments (see AAZ19953-66)
CC encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3
CC polypeptides (see AAY31889-902). It also relates to the construction
CC of chimeric genes encoding all or a portion of a cyclin, in sense
CC or antisense orientation, where expression of the chimeric gene
CC results in altered levels of the cyclin protein in a transformed
CC host cell. This would have the effect of altering the regulation
CC of cell division in those cells. The nucleic acid fragments may be
CC used to express cyclins in plant cells to enhance cell tissue
CC culture growth. The availability of nucleic acid sequences encoding
CC all or a portion of cyclins should facilitate studies of cell cycle
CC in plants, provide genetic tools to enhance cell growth in tissue
CC culture, increase the efficiency of gene transfer and help provide
CC more stable transformations. The proteins can be used as targets
CC to facilitate design and/or identification of inhibitors of those
CC enzymes that may be useful as herbicides.

XX
SQ Sequence 2259 BP; 617 A; 459 C; 523 G; 660 T; 0 other;

Query Match 100.0%; Score 2259; DB 20; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACTTCTCCCACTCATTCATCAACAACACACACACTCTCTCCCTCTGACCA 60
Db 1 ACACTTCTCCCACTCATTCATCAACAACACACACACTCTCTCCCTCTGACCA 60
QY 61 AAACCACTTCTCCGGGACATCTCCGGTCAGGTTCCGGCAACCTCATCGGGAATCGGCA 120
Db 61 AAACCACTTCTCCGGGACATCTCCGGTCAGGTTCCGGCAACCTCATCGGGAATCGGCA 120
QY 121 TGCCACACATGATGCGGAACTCCGCTGCCGCCGCCCTCTCATGTGCTTCCCTG 180
Db 121 TGCCACACATGATGCGGAACTCCGCTGCCGCCGCCCTCTCATGTGCTTCCCTG 180
QY 181 CCTCTCCGACTACGACCTCTCTGCGGAGGACTCTCTCCGGAATCCTCTCCGAGATC 240
Db 181 CCTCTCCGACTACGACCTCTCTGCGGAGGACTCTCTCCGGAATCCTCTCCGAGATC 240
QY 241 GCCGGAGTGTCTCTCTCCGACATCGACTCTCTACCTCTCCGCCGCGGAGACAGA 300
Db 241 GCCGGAGTGTCTCTCTCCGACATCGACTCTCTACCTCTCCGCCGCGGAGACAGA 300
QY 301 GGATTGTATTGATCGATCGCGAGCTTCATCGAGCAGCGCAACTTCGTTCCGGATTGCA 360
Db 301 GGATTGTATTGATCGATCGCGAGCTTCATCGAGCAGCGCAACTTCGTTCCGGATTGCA 360
QY 361 GTAACCTGTGCGGTTCCAATCTCGCTCCCTGAGCGCAACGCCAGAGAAGAACTAGTTGG 420
Db 361 GTAACCTGTGCGGTTCCAATCTCGCTCCCTGAGCGCAACGCCAGAGAAGAACTAGTTGG 420
QY 421 ATGGATTCTCAAGGTACAGCGGTACTATGGCTTTCAGCCTTTGACGGCGTACTCGCCGT 480
Db 421 ATGGATTCTCAAGGTACAGCGGTACTATGGCTTTCAGCCTTTGACGGCGTACTCGCCGT 480
QY 481 CAACTATATGATCGGTTTGGATTCTCGCCGGTTGCCGGAACAATGGGTGGCTCT 540
Db 481 CAACTATATGATCGGTTTGGATTCTCGCCGGTTGCCGGAACAATGGGTGGCTCT 540
QY 541 GCAACTGTATCTGTGATGCTGTCTTTGGCAGCAAAAGATGGAAGAACCTCTGTCTCC 600
Db 541 GCAACTGTATCTGTGATGCTGTCTTTGGCAGCAAAAGATGGAAGAACCTCTGTCTCC 600

Db 541 GCAACTGTATCTGTGATGCTGTCTTTGGCAGCAAAAGATGGAAGAACCTCTGTCTCC 600
QY 601 ATCTCTTTGGACCTTCAGATAGAGGTGCCAAGTACATATTTGAGCCGAGAACAAATCG 660
Db 601 ATCTCTTTGGACCTTCAGATAGAGGTGCCAAGTACATATTTGAGCCGAGAACAAATCG 660
QY 661 TAGGATGAGCTACTTGTCTCGGTGTCTTAGATTGGAGGCTAAGATCACTAACACACT 720
Db 661 TAGGATGAGCTACTTGTCTCGGTGTCTTAGATTGGAGGCTAAGATCACTAACACACT 720
QY 721 TTGCTTCTCGGTTTCTTTGCGTGCAGAGTAGATTCAACTGCACTTTATCCGGTTCT 780
Db 721 TTGCTTCTCGGTTTCTTTGCGTGCAGAGTAGATTCAACTGCACTTTATCCGGTTCT 780
QY 781 TATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAGAGGCTAGCTTCTTGCCTTA 840
Db 781 TATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAGAGGCTAGCTTCTTGCCTTA 840
QY 841 CTGGCCTTCATGATGTGCTGCTGCAGGCATCTCAGCTGAGCTAATGAATTCCTAATTG 900
Db 841 CTGGCCTTCATGATGTGCTGCTGCAGGCATCTCAGCTGAGCTAATGAATTCCTAATTG 900
QY 901 GTCTGTGTTAAGCCCGAAATGCTGATCATGTGCGAGGAGCTAAGAAAAGAAAGT 960
Db 901 GTCTGTGTTAAGCCCGAAATGCTGATCATGTGCGAGGAGCTAAGAAAAGAAAGT 960
QY 961 AATAGGCTGTCCAGCTTGTATGCAAGAGCTTGTGATTAACTAATCAACGGAACCTCCC 1020
Db 961 AATAGGCTGTCCAGCTTGTATGCAAGAGCTTGTGATTAACTAATCAACGGAACCTCCC 1020
QY 1021 CTTACTAAAGTGTGCGCAGCTGCGAGTAAACAATCCGACCCGAATGAGTCAAGTAC 1080
Db 1021 CTTACTAAAGTGTGCGCAGCTGCGAGTAAACAATCCGACCCGAATGAGTCAAGTAC 1080
QY 1081 TGTATCATCATCTCATCATCTCTCTCAACCTCTCTCTCTGTGTGTAAGAGAGGAA 1140
Db 1081 TGTATCATCATCTCATCATCTCTCTCAACCTCTCTCTCTGTGTGTAAGAGAGGAA 1140
QY 1141 ATTAATTAACCGTTTGTGGGTAGATGACAAAGGAACTCCGAGTGAAGAGAAACGAA 1200
Db 1141 ATTAATTAACCGTTTGTGGGTAGATGACAAAGGAACTCCGAGTGAAGAGAAACGAA 1200
QY 1201 ACAATTAATAAAGAGGGAAGAAAGAGGGAATTAAGGTGGGCCAAGTTGTCTAGAA 1260
Db 1201 ACAATTAATAAAGAGGGAAGAAAGAGGGAATTAAGGTGGGCCAAGTTGTCTAGAA 1260
QY 1261 CCTCAACATTTTAAAGAGGTTTAAAGGCAATTAATAATGACTGAGGTGTAGATT 1320
Db 1261 CCTCAACATTTTAAAGAGGTTTAAAGGCAATTAATAATGACTGAGGTGTAGATT 1320
QY 1321 ATAATAGTATATATGATATATCTATCTATCTATATCTAAGAGAGTTGATGGTTGG 1380
Db 1321 ATAATAGTATATATGATATATCTATCTATCTATATCTAAGAGAGTTGATGGTTGG 1380
QY 1381 AGTAATTTTATTTTATGTGTGCTGACTTATTAATTTGAGTTTGCAGAAATTCACCTAGG 1440
Db 1381 AGTAATTTTATTTTATGTGTGCTGACTTATTAATTTGAGTTTGCAGAAATTCACCTAGG 1440
QY 1441 GAAGAGGATTTTGCAGACATGTTACCGTGGGAGAGAGAAATGAGAGAAAGAAAGTGA 1500
Db 1441 GAAGAGGATTTTGCAGACATGTTACCGTGGGAGAGAGAAATGAGAGAAAGAAAGTGA 1500
QY 1501 CACTGAACGAGGGGTAGAGAAATTAATGTGATTTGTTCTGTAACTGTGATTTGAAG 1560
Db 1501 CACTGAACGAGGGGTAGAGAAATTAATGTGATTTGTTCTGTAACTGTGATTTGAAG 1560
QY 1561 GAAAGAAATGAGTTGCGGCTGATTTCAAGTTTGATTAATTACTTGGTGAAGAGAT 1620
Db 1561 GAAAGAAATGAGTTGCGGCTGATTTCAAGTTTGATTAATTACTTGGTGAAGAGAT 1620
QY 1621 GAAAGATGTTGGGGCAACGCTGTAGAGATTGAGAAGAGAGAAAGTAGAGAGAGCTAT 1680
Db 1621 GAAAGATGTTGGGGCAACGCTGTAGAGATTGAGAAGAGAGAAAGTAGAGAGAGCTAT 1680

OY	1681	GAAAAACTCTGGTGATTAATTGAAAGTGAACCTAGAAGTTGAAGTGTCAATGTTTCAT	1740
Db	1681	GAAAAACTCTGGTGATTAATTGAAAGTGAACCTAGAAGTTGAAGTGTCAATGTTTCAT	1740
OY	1741	ATCATGSTATTCATAAGTCAAGCAAAGCTTCATTTCTGGCCAGCATCACGTGCTTCTTCA	1800
Db	1741	ATCATGSTATTCATAAGTCAAGCAAAGCTTCATTTCTGGCCAGCATCACGTGCTTCTTCA	1800
OY	1801	TCATCCACGTTACTACTCTTGGATGGGACCCTCAACAGTAAAGAACAATGCAAGGCCAA	1860
Db	1801	TCATCCACGTTACTACTCTTGGATGGGACCCTCAACAGTAAAGAACAATGCAAGGCCAA	1860
OY	1861	TAA GTTGAAGTTTGGCTACAAATCGTGCACCTTTTTTGTGGGTATTTGGCAGCTGTGCAG	1920
Db	1861	TAA GTTGAAGTTTGGCTACAAATCGTGCACCTTTTTTGTGGGTATTTGGCAGCTGTGCAG	1920
OY	1921	TCG GTTCTGTGCGGTGCCAATGAAGTGTGACGTGATTTTCTTTTCTTGGTTTTC	1980
Db	1921	TCG GTTCTGTGCGGTGCCAATGAAGTGTGACGTGATTTTCTTTTCTTGGTTTTC	1980
OY	1981	TTT GCGGGAGCTGTTAATATATTTTTCCTATTTTGGCCATGAGTTTGGCCTAAC TAT	2040
Db	1981	TTT GCGGGAGCTGTTAATATATTTTTCCTATTTTGGCCATGAGTTTGGCCTAAC TAT	2040
OY	2041	ACAGGACTCCAATGGCTGCTGCCGCGGTGATGGAACACAGTGTATATATAGGTTT	2100
Db	2041	ACAGGACTCCAATGGCTGCTGCCGCGGTGATGGAACACAGTGTATATATAGGTTT	2100
OY	2101	AATTTAAAACCTTGAATTTTATTTGTTTCAAGAGAGAGAACCCTTTCACATA	2160
Db	2101	AATTTAAAACCTTGAATTTTATTTGTTTCAAGAGAGAGAACCCTTTCACATA	2160
OY	2161	GCGGTAAAAGCTTTTGGGGCCTTTTCCGTGTGCTGTGTA TTGGATTGATTAATATAT	2220
Db	2161	GCGGTAAAAGCTTTTGGGGCCTTTTCCGTGTGCTGTGTA TTGGATTGATTAATATAT	2220
OY	2221	AATGACAAC TATTAATTTCTTAAAAAAAAAAAAAAAAAAAAA	2259
Db	2221	AATGACAAC TATTAATTTCTTAAAAAAAAAAAAAAAAAAAAA	2259

RESULT 2	
AAZ19959	
ID	AAZ19959 standard; cDNA; 1994 BP.
XX	
AC	AAZ19959;
XX	
DT	21-DEC-1999 (first entry)
XX	
DE	Soybean cyclin delta-1 cDNA.
XX	
KW	Cyclin delta-1; soybean; cell cycle; cell division;
KW	transgenic plant; herbicide; plant breeding; ss.
XX	
OS	Glycine max.
XX	
FH	Key
FT	1.957
FT	Location/Qualifiers
FT	/*tag= a
XX	
PN	WO948486-A2.
XX	
PD	30-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06047.
XX	
PR	23-MAR-1998; 98US-0078948.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
PI	Cahoon RE, Klein TM, Odell JT, Orozco EM;
XX	

DR	WPI; 1999-591036/50.
DR	P-PSDB; AAZ31895.
XX	
PT	New isolated plant cyclin genes, used to develop products for use as
PT	herbicides and for developing plant breeding programs -
XX	
PS	Claim 7; Page 53-54; 68pp; English.

This nucleotide sequence represents a portion of the cDNA insert in clone se6.pk0028.fl1 encoding a portion (see AY31895) of a soybean cyclin delta-1 protein. The clone was isolated from a soybean embryo (26 days after flowering) cDNA library. The invention relates to isolated nucleic acid fragments (see AA219953-66) encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see AY31889-902). It also relates to the construction of chimeric genes encoding all or a portion of a cyclin, in sense or antisense orientation, where expression of the chimeric gene results in altered levels of the cyclin protein in a transformed host cell. This would have the effect of altering the regulation of cell division in those cells. The nucleic acid fragments may be used to express cyclins in plant cells to enhance cell tissue culture growth. The availability of nucleic acid sequences encoding all or a portion of cyclins should facilitate studies of cell cycle in plants, provide genetic tools to enhance cell growth in tissue culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets to facilitate design and/or identification of inhibitors of those enzymes that may be useful as herbicides.

Sequence 1994 BP; 534 A; 361 C; 477 G; 622 T; 0 other;

Query Match	30.5%;	Score 689.6;	DB 20;	Length 1994;
Best Local Similarity	67.0%;	Pred. No. 1e-163;		
Matches 1363;	Conservative	0;	Mismatches 519;	Indels 152;
				Gaps 21;

QY	287	TCGCCGACGACAGAGCATGTGTTATTCTGCATCGCGAAGCTTCAATCGACGACGAGCGCAACTTC	346
Db	52	TCCTCGCCGCCGCTCGGAGGGCGGAGTCCATCGCCGGATTCAATGGAAGACGAGCGCAACTTC	111
QY	347	GTTCCGGGATTGCGATPACCTGTGCGCGGTCCAATCTCGCTCCTCGAACGCCAACGCCAGA	406
Db	112	GTTCCCCGATTTCGAATACCCTCAATAGGTTCCAATCTCGCTCTCTGACAGCCTCTGCCAGA	171
QY	407	GAAGAAATCAGTTGGATGGATTCTCAAGGTACACGCCGTACTATGGCTTTCAGCCTTGACG	466
Db	172	GAAGAAATCCGTTGCATGGATTCTCAAGGTGACGGCTTATTACGCTTTTCAACCCGGTCAAG	231
QY	467	GCGTACCTCGCCGTCACAATAATATGATCGGTTTTTTGGATTCTCGCCGGTT--GCCGGA	523
Db	232	GCTTATCTTCCGTTAACTACTTGGATAGGTTCTTGAATTCTCGACCGTTGCCGCCGAAA	291
QY	524	ACAAATGGGTGGCCCTCTGCCAACTTGTAATCTGTGCATGCTTGTCCTTTGGCAGCAAAGATG	583
Db	292	ACGAATGGGTGGCACATGCAACTTCTCTGTGTGCGTGCTTGTCCTTAGCAGCAAAGATG	351
QY	584	GAGAAACCTCTGTTCATCTCTCTTGGACCTTCAGATAGAAAGTCCAAAGTACATATTT	643
Db	352	GAGGAATCTCTAGTTCATCTCTTTTGACCTTCAGGTAGAAAGTCTAATAATACGTATTT	411
QY	644	GAGCCGAGAACAAATTCGTAGGATGGAGCTACTGTCTCGGTGTCTTAGATTGGAGGCTA	703
Db	412	GAACCCAAACAATTAGAAGAATGGAGCTACTGTCTTGCGCGGTGTGGATTGGAGGCTA	471
QY	704	AGATCAGTAAACACCACCTTGTCTCTCGCTTCTTTGGCGTGCAAAAGTAGATTCAACTGGA	763
Db	472	AGATCGGTTACCCCATTAGCTTCTCTCGATTCTTTGCGTGCAAGTTAGATTCAACTGGG	531
QY	764	ACTTTATCCGGTCCATTATTTCCAGGGCAAGAAATCATGTAATCTAATATCCAAAGG	823
Db	532	ACTTTTACCGGTTCCATCTTACAGTGTGCTACACAATAATTACTTAATATACAAAGG	591
QY	824	GCTAAGCTTCTTGTGTTACTGGCCTTCATGCAATGTGCTGTGACGCCAATCACTCAGCT	883

Db 592 GCTAGCTTCTTGGCTATTTGGCCATCATGCATTTGCTGCAGACCCATTTCTCCATGCAGCA 651
QY 884 AATGAATTCCTAATTTGCTGCTGCTTAAGCCCGAAAAATGCTGAGTCATGTCGAGGGA 943
Db 652 AATGAATTCCTAATTTGCTGCTGCTTAAGCCCTGAGCATGCAGTCATGTCGTGAGGGG 711
QY 944 CTAGAAAAAGAAAGTAATAGGGTCTACCAGTTGATGCCAAGACCTTGATTAACAAT 1003
Db 712 TTAAAGAAAGAAAAATTATAGGGTCTACCAATTAATGCAGAACTTGATTGACAAT 771
QY 1004 AACCAACGGAACCTCCCTTACTAAAGTGTGCCGAGCTGCGAGTAACAA--CTCGG 1060
Db 772 AACCAAGAGAAACCCCC-----TAAGGTGTTACACAGCTGCGAGTACAATATCTCGG 825
QY 1061 ACCCGAATGAGGTCAAGTACTGATCATCTCTCATCATCCTCTTCA---ACCTCCTTC 1117
Db 826 CCCATTAAGAGTCTAGTGTCTCATCTCTCTTAGCATCATCTCTCACCTTCATCATCC 885
QY 1118 TCCCTGCTTTGTAAGAGGAGGAATTAATAACCGTTTGTGGTA--GATGACAAAGGA 1174
Db 886 TCTTTGCTTTGTAAGAGGAGGAATTAATAAATCTTTGTGGTAGACGATGACAAAGGA 945
QY 1175 AACTCCGAGTGAAGAAAAAGAACACAAATAATAAAGAGGGAAGA-----AAA 1225
Db 946 AACTCCCAATGAAGAAAAAGAACCAATTAATAGAGGAAAAAAGAAAGAAATTAATGAAA 1005
QY 1226 AGAGAGGAATAGGTGGGCCAAGTTGTTCTGTAACCTCAACATTTTGAAGGGTTT 1285
Db 1006 TAAGTGGTGAAGGGTGTCCAAAGTTGTCCAGAAACCGCAAAATTTTAAAGGGTTT 1065
QY 1286 GCAATTAATAATGACTT---GAGTGAGGGTGTAGATTATATAGTATATATGATATA 1342
Db 1066 TTGAGTATAAATGAGACTAGAGAGTCGAGGTGTACATTAATAATAGACTATATTTATG 1125
QY 1343 TCTCTATCGTATATACTAAGAGAGTTGATGGCTTTGAGTAATTTTATTTATGTTG 1402
Db 1126 A-----GAGTTGCGAGCTTTTATTTATTTGTTGTTG 1156
QY 1403 GTGACTTATTAATATGAGTTTGCAGAATTCACCTAGGGAAGAGGATTTTGCACATGT 1462
Db 1157 GGTGTTGCCATTCATCATGCAATGCAATTCAGATTCCTTAGGGAAGGATTTTGCAAAGTGT 1216
QY 1463 TACCGTGGAGAGGAATGAGAGAAGAAAGAGTGAACACTGAACCAAGGGGTAGAGAA 1522
Db 1217 GTGTGGGTGTCGTGAGAGAGAGGTGGGAATTAAGATACAAAGATGCAT----- 1265
QY 1523 TTTAATGTGATTTGTTCTTGTAACTGTGATTTCTGAAGCAAAAGAAATTGAGTTGCGGCTG 1582
Db 1266 -----TTAATGGTTTGGTCTGTCAAGCGTGAAGAAAGAAAGTGT---TGTAGTTTG 1312
QY 1583 GATTTCAAAAGTTTGCATTAATTAATCTTGTGTAAGAGAGATGAAGATGTTGGGGCAACGCT 1642
Db 1313 GAATTCAAAAGATGCGCTT--GTATTTGGTGAAGAGAAAGAAATGTTGGTGGACATGTC 1370
QY 1643 GTAGAGATTGAGAAGAAAGTAAGAGAGAAGGTATGAAAAACCTGTGATTATTTGA 1702
Db 1371 TTCAGAGCTTGAAGAGAAAGAAAGCATAGTCTCAGAGCAGATATCAATAGGSTATTGA 1430
QY 1703 AAGTTGAAACTTGAAGTTTGAAGTGTTCATGTTCATATCATGTTGATTCATAAGTCAAG 1762
Db 1431 AAG-----ACTTTGAAGTTTGAAGCTGTTTCTTCTTATTAATATGAGGGTCTCTAAGTCAAG 1485
QY 1763 CAAAGCTTCATTTCTTGGCCAGCATCTGCTTCTTCATCATCCAGTTACTACTT 1822
Db 1486 CTACTCATCTTGGCCA--GCATGCTTCGCTTCTTCAAGTTTACAGCTTACTTTTGGTAGTGT 1544
QY 1823 GATGGGACCCCTCAACAGTAAGAACAATTGAAGGCAATTAAGTTGAAGTTTGGCTACAAA 1882
Db 1545 GATGGGATACCACTAGAGTACAAAAAAGAAATAAGCAATAAGTGAATCTTATC-ACATTT 1603
QY 1883 TCGTGAAGCTTTTGTGTTGGGTATTTGGCAGCTGTGCAGTCGGTTCTGCTGCGTGCATG 1942
Db 1604 TTGTGAGCTTAATGATGATACGTGT-----GAGACGCTCTCTGTTGTGTCTCGC 1652

QY 1943 AAGTGTACGTGTGATTTTCTTTTCTTGCTTTT-----TCCTTTCGGGAGCTGT 1996
Db 1653 ACGTGCCACGTGTGATTTTATTTATTTATGTTTAACTAAGCCGGAATGCTTT 1712
QY 1997 ATATATTTTTCCTATTTTGGCCATGAGTTTGGCCTAACCTATACAGACTCCAATGGC 2056
Db 1713 TTATTTCTTATTTCTTTTGGCTTGAGCTTTGGCCTAACCTATACAGGA-TCCATTTGCC 1771
QY 2057 TGGTGTCCGCGGTGTGATGGAACACGCTGTATATATAGTTTAAATTAACCTGA 2116
Db 1772 TGGTGTCCAGC--GTGATGGAACACGCTGTCTATA---GTTTCAATTTTGTGTTGG 1825
QY 2117 ATTTTATTTTGTGTTTCAAGAGAGAGAGAACCTCTTT----- 2154
Db 1826 ATTTTTCATTTGTTTCAAGAGAGAGAACCTCTTTTGTGTTTCTTTTAACTGCTAAT 1885
QY 2155 -----CACATAGGGGTAAAGGTCTTGGGCTTTTTCCTGTGCTGTGATTTG 2205
Db 1886 TGGCTTTGGAGAAATTGAGATAAGCGCTTTGGGGCTTTTCCGTGAGTCTTTGTATTG 1945
QY 2206 GATTGATTAAATATTAATGACAACCTATTAATTTCTTAAAAAAAAAAAAAAA 2259
Db 1946 AATTCATTAAATATGA-----CACTGTTAATTTCTATAAAAAAAAAAAAAA 1994

RESULT 3
AAC42423
ID AAC42423 standard; DNA; 1337 BP.
XX
AC AAC42423;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35500.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.

PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 17.2%; Score 388.4; DB 21; Length 1337;
Best Local Similarity 68.9%; Pred. No. 8.4e-88;
Matches 565; Conservative 0; Mismatches 246; Indels 9; Gaps 2;

QY 297 CAGAGATTGTATTGATCGGCGAGCTTCATCGACGACGCGCAACTTCGTTCCGGAT 356
DB 289 CATGGCCCTGGTGATTCATCGCTTGTTTATCGAAGACGAGCGTCACTTCGTTCCGGAC 348
QY 357 TCGAGTACCTGTCCGGGTCCCAATCTCCCTCCCTGGACGCCAACGCCAGAGAAGATCAG 416
DB 349 ATGATTATCTCTCTAGATTTCAAACTCGATCTCTCGATGCTCCGCTAGAGAAGATTCCG 408
QY 417 TTGGATGATCTCTCAAGGTACACGCGTACTATAGCCTTTCAGCCCTTTCAGCGCGTACCTCG 476
DB 409 TCGCATGGAATTCTCAAGGTACAAAGCGTATTAACTTTCAGCCCTTTCAGCGCGTACCTCG 468
QY 477 CCGTCAACTATATGATCGGTTTTTGATTTCTCCGCGGTGCGGAAACAATGGGTGGC 536
DB 469 CCGTTACTATATGATCGGTTTCTTACGCTCGTCCGATTACCGGAACGAGTGGTGGC 528
QY 537 CTCTGCAACTGTATCTGTGTCATGCTGCTTTTGGCAGCAAGATGAGAACCTCTTG 596
DB 529 CAATGCAACTTTTAGCAGTGGCATGCTGTCTTTAGCTGCAAGATGAGGAATTTCTCG 588
QY 597 TTCATCTCTCTGGACCTTCAGATAGAAAGGTGCCAAGTACATATTTGAGCCGAGAACA 656
DB 589 TTCTTCTCTTTTGAATTTTCAGGTTGACGAGTGAAGTATTATTGAGCAAAAACCTA 648
QY 657 TTCTGATGAGGAGTACTTGTCTCGGTGCTTAGATTGGAGGCTAAGATCAGTAACAC 716
DB 649 TAAAAAGAAATGAACTTCTGTCTTAAGTGTGTTAGATTGAGACTAAGATCGGTTACAC 708
QY 717 CACTTGTCTCTCCGCTTTCTTTGCGTGAAGTAGATTCAACTGGAACCTTTTATCCGCT 776
DB 709 CGTTGATTTTCATGCTTCTTGTCTTACAGATCGATTCCTTCGGGTACCTTCTCGGGT 768
QY 777 TCCTTATTTCCAGGCAACAGAAATCATCGTATCTAATATCCAGAGGCTAGCTTTCTG 836
DB 769 TCTTTATCTCCCATGCTACAGAGATTATCTCTCAACATTAAGAAAGCGAGCTTTCTTG 828
QY 837 CTTACTGGCTTCATGCTATGCTGCTGACGCCATCACTGACGTAATGAATTCCTA 896
DB 829 AGTACTGGCCATGAGTATAGCTGACGCCGATTCCTGTGTAGCGAAAGAGTTACCTT 888
QY 897 ATTGGTC-----TGTGGTTAAGCCCGAAAAATGCTGAGTCAATGCTGCGAGGAGCTAAGAA 950
DB 889 CTCTATCTCTGTGTGTCATCCCCACGAGAGCCCTGAGACTTGGTGTGACGAGATTGACA 948
QY 951 AAGAAAAAGTATAGGGTGTACCAAGTGTGATGCAAGAGCTTGTGATTACATATACCAAC 1010
DB 949 AAGAGAAAGATAGTAGATGCTATAGACTGATGAAGCAATGGCCATCGAGAATTAACCGT 1008
QY 1011 GGAACCTCCCTTACTTAAAGTGTGCGCGAGCTGCGAGTAA--CAACTCGAGCCGAA 1067
DB 1009 TAAATACACCAAAAGTATAGCAAAAGCTTCGAGTGAAGTAAAGGCGATCATCGACGTTAA 1068
QY 1068 TGAGGTCAAGTACTGTATCATCATTTCTCATCATCTCTTC 1107
DB 1069 CAAGGCCAAGTGAATCTCTTCTCATCTCTCTCC 1108

RESULT 4
AAV33887

ID AAV33887 standard; cDNA to mRNA; 1788 BP.

XX AC AAV33887;

XX DT 25-JAN-1999 (first entry)

XX DE H.tuberosus CYCD1;1 gene.

KW D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.

XX OS Helianthus tuberosus.

XX PN W09842851-A1.

XX PD 01-OCT-1998.

XX PF 24-MAR-1998; 98MO-EP01701.

XX PR 26-MAR-1997; 97EP-0302096.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PI Murray JAH;

XX DR WPI; 1998-532012/45.

XX PT Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.

XX PS Claim 14; p56-57; 75pp; English.

XX CC This sequence represents the CYCD1;1 cDNA from Helianthus tuberosus which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.

XX SQ Sequence 1788 BP; 511 A; 386 C; 387 G; 504 T; 0 other;

Query Match 16.8%; Score 379.8; DB 19; Length 1788;
Best Local Similarity 72.5%; Pred. No. 1.4e-85;
Matches 492; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 307 TTAATTGATCGCGAGCTTCATCGAGCAGCGCAACTTCGTTCCGGATTGAGTACCT 366
DB 284 TGATTGATCGCGGAGTTTATGAACAAGAGAGAAAGTTGTTCCAGGAATCGATTACGT 343
QY 367 GTCCGGGTTCCAAATCTCGCTCCCTGGACGCCCAACGCCAGAGAAGATCAGTTGATGAT 426
DB 344 CGAGCGATTTCAATCGCAAGTTCTCGATGCTTCTGCTAGACAAGATCGTTGCCCTGAT 403
QY 427 TCTCAAGGTACACGCGTACTATGCTTTCAGCCCTTTGACGGCGTAACTCGCCCTCACTA 486
DB 404 CCTTAAGGTGCAACGGTTTTCAGGATTTTCAGCCGTTGACGGCGTAACTCTCCGTTACTA 463
QY 487 TATGATTCGGTTTTTGGATTTCTCGCCGCTTGCCGAAACAATGGGTGGCTCTGCAACT 546
DB 464 TCTGATCGTTTCATCATATTGCCGTGGCTTCCCGTGGCAAAATGGGTGGCCCTGCAACT 523
QY 547 TGTATCTGTGATGCTGTGTCTTTGGCAGCAAAAGATGGAAGAACTCTGTTCATCTCT 606
DB 524 CTATCTGTAGCATGCTGTGTCTTTAGCTGCTTAAATGAGGAAACCCTTATTCCTTCTAT 583

OY	607	CTTGACCCCTTCAGATGAGAAGGTGCCAAGTACATATTGGAGCCGGAACAATTGCGTAGGAT	666
Dd	584	TCTTGATCTCCAGGTTGAAGGTGCAAAATATATTTTCGAGCCGAAACCAATCCGAAGAAAT	643
OY	667	GGAGCTACTGTGTTCTCGGTGCTTGAATTTGAGAGCCTAAGATCATGAACACACTTTGCTT	726
Dd	644	GGAGTTCTGTGCTTAGTGTGTTGGATTGGAGACTAAGATCCGTTACACCGTTTAGCTT	703
OY	727	CCTCGCTTTCTTTGCGTGCACAAAGTAGATTCAACTGGAACCTTTATCCGGTTCCTTAATTC	786
Dd	704	TATCGGCTTCCTTTCCGACAAAAATGCATCCATCTGGAATGATATACGGGTTTCCTTAATCTC	763
OY	787	CAGGCAACAGAAATCATCGTATCTAATATCCAAGAGGCTAGCTTCTTGCTTACTGGCC	846
Dd	764	AAGGGCACACAAATATATCTCTCTCAATATTCAGAAGCTACTTACTTGAGATTTGGCC	823
OY	847	TTCATGCATTCGTCTGCTGCAGCCATTACTCACTGCAGCTAATGAATAATTCCTAATTTGGTCTGT	906
Dd	824	ATCATGTATTCGTCTGCTGCACACAATACTTTGTGCAAGCAAGTATCTTCTAATTTCTCACT	883
OY	907	GGTAAAGCCCCAAAATGCTGAGTCAATGCTGCGAGGAGCTAAGCAAAAAGAAAGTAAATAGG	966
Dd	884	TATCAATGCTGATCATGCTGTAATCATGTGTGATGGCCCTTAGCAAAAGAGAAGATCACAA	943
OY	967	GTGCTACCAGTTGATGCCAA	985
Dd	944	ATGTTACAGACTTGTACAA	962

RESULT 5	
ID	AAV33885 standard; cDNA to mRNA; 1679 BP.
XX	AAV33885
AC	AAV33885;
XX	
DT	25-JAN-1999 (first entry)
XX	
DE	N. tabacum CYCD3;1 gene.
XX	
KW	D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW	CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KM	root development; ds.
XX	
OS	Nicotiana tabacum.
XX	
PN	W09842851-A1.
XX	
PD	01-OCT-1998.
XX	
PF	24-MAR-1998; 98WO-EP01701.
XX	
PR	26-MAR-1997; 97EP-0302096.
XX	
PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX	
PI	Murray JAH;
XX	
DR	WPI; 1998-532012/45.
XX	
PT	Regulating growth and structure of plants by modulating protein that
PT	controls cell division - specifically a D-type cyclin, and related
PT	chimeric genes and transformed cells and plants, used to alter
PT	growth rate, flowering, seed production etc.
XX	
PS	Claim 14; p54; 75pp; English.
XX	
CC	This sequence represents the CYCD3;1 cDNA from Nicotiana tabacum which
CC	encodes a D-type cyclin. The sequence can be used to alter the growth
CC	characteristics or architecture of plants by altering the (functional)
CC	level in the plant cells of a cell-division controlling protein that can
CC	bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC	Modulation of the cyclin gene is used to increase or decrease the growth
CC	rate, provide faster germination, reduce time to flowering, increase the

CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
XX
SQ Sequence 1679 BP; 537 A; 281 C; 293 G; 568 T; 0 other;

Query Match	6.8%;	Score 152.6;	DB 19;	Length 1679;
Best Local Similarity	52.2%;	Pred. No. 3e-28;		
Matches 338;	Conservative	0;	Mismatches 309;	Indels 0;
			Gaps	0;

[illegible]

RESULT	6
AAV33888	
ID	AAV33888 standard; CDNA to mRNA; 1414 BP.
XX	
AC	AAV33888;
XX	
DT	25-JAN-1999 (first entry)
XX	
DE	H.tuberosus CYCD3;1 gene.
XX	
KW	D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW	CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW	root development; ds.
XX	
OS	Helianthus tuberosus.
XX	
PN	W09842851-A1.

XX 01-OCT-1998.
PD
XX 24-MAR-1998; 98WO-EP01701.
PF
XX 26-MAR-1997; 97EP-0302096.
PR
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Murray JAH;
XX
DR WPI; 1998-532012/45.
XX

PT Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.

PS Claim 14; p58; 75pp; English.

XX This sequence represents the CYCD3;1 cDNA from Helianthus tuberosus which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.

XX Sequence 1414 BP; 449 A; 276 C; 248 G; 441 T; 0 other;

Query Match 5.9%; Score 134.4; DB 19; Length 1414;
Best Local Similarity 51.7%; Pred. No. 1.le-23;
Matches 306; Conservative 0; Mismatches 286; Indels 0; Gaps 0;

OY 401 GCCAGAGAAGAAATCAGTTGGATGATTCCTCAAGGTACACGCGTACTATGGCTTTACGCT 460
DB 321 GCTCGTAAGAGGCGTGTAGATTGATCCTTAAGGTCAAAAGTTGTTATGATGCATCACACCT 380
OY 461 TTGACGGCGTACCTCGCCGTCACACTATATGATGATCGTTTGGATTCTCGCGGTTGCCG 520
DB 381 CTTACAGCCATTTTAGCCATCAATTATCTGTGATAGGTTTCTTCTAGCCCTCCATTTTCAA 440
OY 521 GAAACAAATGGGTGCTCTGCAACTGTGATCTGTTCATGCTTGTCTTTGGCAGCAAAG 580
DB 441 GAAGATAAACCTTGATGATTCAACTGTGCTGTAGTGTCTCTCTTTAGCTGTCTAAA 500
OY 581 ATGGAAGAACCTTGTTCATCTCTCTTGACCTTCAGATAGAAGGTGCCAAGTACATA 640
DB 501 GTTGAAGAACCTCAAGTGCACCTTACTAGATCTTCAAGTAGAGACACTAAGTACTTG 560
OY 641 TTTGAGCCGAGAACATTCGTAGATGAGCTACTGTCTCGGTGTCTTAGATTGGAGG 700
DB 561 TTTGAGGCTAAAAACATACAAAAAATGGAGCTTTTGGTATGTCAACTTTGAATGGAGG 620
OY 701 CTAAGATCAGTAACACCACTTTGCTCTCGCTTCTTTCCTTTCGCTGCAAGTAGATTCACT 760
DB 621 ATGAACCCAGTGACACCAATCTCATTTCTTGATCACATTTGAAGAAGGCTTGATTACT 680
OY 761 GGAACCTTTATCCGTTCCCTTATTTCCAGGGCAACAGAAATCATCGTATCTAATATCAA 820
DB 681 GATCATGTTTCAATGGGATTTTTCAGAAGATGTGAAGCTATGATCCTTTGTTAGTTTCA 740
OY 821 GAGGCTAGCTTCTTGTCTTACTGGCCTTCATGATGCTGCTGCACCATACTACTGCA 880
DB 741 GATTCAAGATTCGTGTGTATATAACCATCCGTTGTGGCCACAGCTACAATGCTTCACGTT 800
OY 881 GCTAATGAATTCCTAATTGGTCTGTGTAAAGCCGAAATGCTGAGTCATGTGCGAG 940
DB 801 GTAGATGAATTTGATCCTCCCAATTGTATTGACTACAAAAGTCAACTTCTGGAATCTTCTC 860

OY 941 GGACTAGAAAGAAAAGTAATAGGCTGCTTACCAAGTTGATGCAAGACTTG 992
DB 861 AAAACCACTAAGACGACGACATTAACGAGTGTACGAGCTCATTTGTCGAGCTAG 912

RESULT 7

AAC40202
ID AAC40202 standard; DNA; 1311 BP.

XX AAC40202;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 27437.

DE Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.

PR	17-JUN-1999;	990S-0139492.
PR	18-JUN-1999;	990S-0139454.
PR	18-JUN-1999;	990S-0139455.
PR	18-JUN-1999;	990S-0139456.
PR	18-JUN-1999;	990S-0139457.
PR	18-JUN-1999;	990S-0139458.
PR	18-JUN-1999;	990S-0139459.
PR	18-JUN-1999;	990S-0139460.
PR	18-JUN-1999;	990S-0139461.
PR	18-JUN-1999;	990S-0139462.
PR	18-JUN-1999;	990S-0139463.
PR	18-JUN-1999;	990S-0139750.
PR	18-JUN-1999;	990S-0139763.
PR	21-JUN-1999;	990S-0139817.
PR	22-JUN-1999;	990S-0139899.
PR	23-JUN-1999;	990S-0140353.
PR	23-JUN-1999;	990S-0140354.
PR	24-JUN-1999;	990S-0140695.
PR	28-JUN-1999;	990S-0140823.
PR	29-JUN-1999;	990S-0140991.
PR	30-JUN-1999;	990S-0141287.
PR	01-JUL-1999;	990S-0141842.
PR	01-JUL-1999;	990S-0142154.
PR	02-JUL-1999;	990S-0142055.
PR	06-JUL-1999;	990S-0142390.
PR	08-JUL-1999;	990S-0142803.
PR	09-JUL-1999;	990S-0142920.
PR	12-JUL-1999;	990S-0142977.
PR	13-JUL-1999;	990S-0143542.
PR	14-JUL-1999;	990S-0143624.
PR	15-JUL-1999;	990S-0144005.
PR	16-JUL-1999;	990S-0144085.
PR	16-JUL-1999;	990S-0144086.
PR	19-JUL-1999;	990S-0144325.
PR	19-JUL-1999;	990S-0144331.
PR	19-JUL-1999;	990S-0144332.
PR	19-JUL-1999;	990S-0144333.
PR	19-JUL-1999;	990S-0144334.
PR	19-JUL-1999;	990S-0144335.
PR	20-JUL-1999;	990S-0144352.
PR	20-JUL-1999;	990S-0144632.
PR	20-JUL-1999;	990S-0144884.
PR	21-JUL-1999;	990S-0144814.
PR	21-JUL-1999;	990S-0145086.
PR	21-JUL-1999;	990S-0145088.
PR	22-JUL-1999;	990S-0145085.
PR	22-JUL-1999;	990S-0145087.
PR	22-JUL-1999;	990S-0145192.
PR	22-JUL-1999;	990S-0145198.
PR	23-JUL-1999;	990S-0145145.
PR	23-JUL-1999;	990S-0145218.
PR	23-JUL-1999;	990S-0145224.
PR	26-JUL-1999;	990S-0145276.
PR	27-JUL-1999;	990S-0145913.
PR	27-JUL-1999;	990S-0145918.
PR	27-JUL-1999;	990S-0145919.
PR	28-JUL-1999;	990S-0145951.
PR	02-AUG-1999;	990S-0146386.
PR	02-AUG-1999;	990S-0146388.
PR	02-AUG-1999;	990S-0146389.
PR	03-AUG-1999;	990S-0147203.
PR	04-AUG-1999;	990S-0147204.
PR	05-AUG-1999;	990S-0147302.
PR	05-AUG-1999;	990S-01477192.
PR	05-AUG-1999;	990S-0147260.
PR	06-AUG-1999;	990S-0147303.
PR	06-AUG-1999;	990S-0147416.
PR	09-AUG-1999;	990S-0147493.
PR	09-AUG-1999;	990S-0147935.
PR	10-AUG-1999;	990S-0148171.
PR	11-AUG-1999;	990S-0148319.
PR	12-AUG-1999;	990S-0148341.
PR	13-AUG-1999;	990S-0148565.

PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149125.
PR	18-AUG-1999;	99US-0149476.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149930.
PR	23-AUG-1999;	99US-0149932.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151066.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158293.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159684.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match	5.4%;	Score 122;	DB 21;	Length 1311;
Best Local Similarity	50.2%;	Pred. No. 1.4e-20;		
Matches 302; Conservative	0;	Mismatches 300;	Indels 0;	Gaps 0;

QY 404 AGAAGAATCAGTTGGATGATTCTCAAGGTACACGGTACTATAGCGTTTCAGCCTTTG 463
|| ||| | ||| ||| | ||| ||| |||
Db 451 AGAAGAAGAGGCTTAGATTGGGTTCTTAGGGTAATACTCATATATGGGTTTACTTCATTG 510

QY 464 ACGGCGTACCCTGCCGTCACATATATGATCGGTTTTTGGATTCTCGCCGGTTGCCGAA 523
||||

Db 511 ACGGCTAATCTGCTGTGAACTACTTCGATAGGTTTATGACAAGTATATAAGCTTCAGACT 570
QY 524 ACAATATGGTGGCTCTGCAACTGTATCTGTTCATAGCTTGTGCGAGCAAAAGATG 583
Cc 571 GATAAGCCATGATGCTCTCAGCTGTGCTGGCTCTTGTCTTAGCTGCTAAAGTT 630
Db 584 GAAGAACCTCTGTTCATCTCTCTGGACCTTCAGATAGAGGTGCCAAGTACATATT 643
Cc 631 GAAGAGATTCAGTTCATGCTCTTAGACCTCCAGTGAAGAAAGCAAGATATCTCTT 690
QY 644 GAGCCGAGAACAAATCGTAGATGAGCTACTGTCTCGGTCTTAGATTGAGGCTA 703
Cc 691 GAAGCTAAGACGATTCAAAGAATGAGCTTTGATTTCTTCTACTCTTCAATGAGAATG 750
QY 704 AGATCAGTAACACCACTTGTCTCTCGCTTCTTTCGCTGCAAGTAGATTCAACTGGA 763
Db 751 CACCCTGTGACTCCAACTCTTCTTGTGATCACAATATCCGGGATTTGGCTCTAAATGG 810
QY 764 ACTTTATCCGGTTCCTTAATTTCCAGGGCAACAGAAATCATCGTATCTAATATCCAAGAG 823
Db 811 CACCAGCAATTAGACTTCTGTAGGAAGTGTAGCGCTTCTGTATCTCTGTATTGCTGAT 870
QY 824 GCTAGCTTTCTGTCTTACTGGCCCTTCATGCAATGCTGCTGCAAGCCATCTACCTGCACT 883
Db 871 ACGAGGTTTATGAGTACTTCCCTTCTGTCTTAGCTACTGCAATATGATCCTTGTCTTC 930
QY 884 AATGAATTCCTAATGTGCTGTGTTAAGCCCGAAATGCTGAGTCATGTGTCGAGGGA 943
Db 931 GAGGAATTCGAAGCCATGTGATGAAGTGAATACCAATCTCAAAATAAGACTCTACTCAAA 990
QY 944 CTAAAGAAAAGAAAAGTAAAGGCTCTACCACTGTGATGCAAGAGCTTGTGATTAACAAT 1003
Db 991 GTCAATCAGAGAGAAAGTAAATGAATGCTATGAACCTGTGTGAGACACAATCCAAGCAAG 1050
QY 1004 AA 1005
Db 1051 AA 1052

RESULT 8

AAV33886
ID AAV33886 standard; cDNA to mRNA; 1431 BP.

XX AC AAV33886;

XX DT 25-JAN-1999 (first entry)

XX DE N. tabacum CYCD3;2 gene.

XX KW D-type cyclin; growth; plant; cell-division control; phosphorylation;

KW CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;

KW root development; ds.

XX OS Nicotiana tabacum.

XX PN WO9842851-A1.

XX PD 01-OCT-1998.

XX PF 24-MAR-1998; 98WO-EP01701.

XX PR 26-MAR-1997; 97EP-0302096.

XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.

XX PI Murray JAH;

XX DR WPI; 1998-532012/45.

XX PT Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.

XX PS Claim 14; p55-56; 75pp; English.
XX CC This sequence represents the CYCD3;2 cDNA from Nicotiana tabacum which
Cc encodes a D-type cyclin. The sequence can be used to alter the growth
Cc characteristics or architecture of plants by altering the (functional)
Cc level in the plant cells of a cell-division controlling protein that can
Cc bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
Cc Modulation of the cyclin gene is used to increase or decrease the growth
Cc rate, provide faster germination, reduce time to flowering, increase the
Cc number of flowers, seeds or fruits per plant, increase root development,
Cc reduce height and to delay flowering in a range of plants, e.g. legumes,
Cc grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
Cc carnation, chrysanthemum, rose, tulip, etc.

XX SQ Sequence 1431 BP; 387 A; 267 C; 299 G; 478 T; 0 other;

Query Match 5.3%; Score 120.8; DB 19; Length 1431;
Best Local Similarity 50.2%; Pred. No. 2.9e-20;
Matches 299; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

QY 399 ACGCAGAGAGAAATCAGTTGATGATTTCTCAAGGTACACGCGTACTATGGCTTTCAGC 458
Db 463 AGGTTAGAAAAGAGGCAATGGATGGATGTTGAGAGTCAATGCTCACTATGTTTCACATG 522
QY 459 CTTTGACGGCGTACCTCGCCGTCATATATGATCGGTTTGGATTCTCGCCGGTTCG 518
Db 523 CTATGACTGCTGTTTAGCTGTGAATTAATTTGATAGTTGATCTGACTCTGCTTTC 582
QY 519 CGGAACAATGGGTGGCTCTGCAACTTGTATCTGTGCAATGCTTGTGGCAGCAA 578
Db 583 AGAAGATTAAGCCTTGGATGATGATCACTGCTGCTGCGCTTCTTCTATGCTGCTGA 642
QY 579 AGATGAGAGAACCTCTTGTTCATCTCTTGGACCTTCAGATAGAAAGTGCCAAAGTACA 638
Db 643 AAGTGAAGAGACCCCAAGTCCCTTCTTGAACCTCCAAAGTGGCTGATTCAGATTTTG 702
QY 639 TATTTGAGCCGAGAACCAATTCGTAGATGAGCTACTTGTTCGCTGCTTAGATTGGA 698
Db 703 TGTTTGAGGCAAGAACTATTCAGAGAAATGGAACCTCTGTGCTCTCCACTCTTAAGTGA 762
QY 699 GGCTAAGATCAGTAACACCACTTGTCTTCCCTTCTTGTGCGTAAAGTAGATTCAA 758
Db 763 AATGAATCCAGATGACACCACTATCTTCAATGATCATATCAGAGAGATTGGATTCA 822
QY 759 CTGGACTTTTATCCGGTTCCTTATTTCCAGGGGCAACAGAAATCATCGTATCTAATATCC 818
Db 823 TGACCAATCTACATTTTGATTTTCTTAGAGAGATGGAAGCGCTCATCTTGGTATTATCA 882
QY 819 AAGAGGCTAGCTTTCTTGTCTTACTGGCCCTTCATGCAATGCTGCTGCAAGCATCACTG 878
Db 883 CTGATTTAGGCTCTTGCAATATCTCCATCTGTTATTGCAACTGCAAGTATGTTTCG 942
QY 879 CAGCTAATGAATTCCTAATTTGCTGTGTTAAGCCCGAAATGCTGAGTCATGCTGCG 938
Db 943 TGATCAATGAGATGAGCCTTGCAATGCAATGGAATACAGAAATCAGTCACTGCTGTC 1002
QY 939 AGGACTAAGAAAAGAAAAGTAAATAGAGGTGCTACCACTGATGCAAGAGCTTGTG 994
Db 1003 TTAAAGTCAAAACAGAGATAGTTTGAAGAATGCCATGATCTTATCTAGAGCTAATG 1058

RESULT 9

AAV33884
ID AAV33884 standard; cDNA to mRNA; 1284 BP.

XX AC AAV33884;

XX DT 25-JAN-1999 (first entry)

XX DE N. tabacum CYCD2;1 gene.

XX KW D-type cyclin; growth; plant; cell-division control; phosphorylation;

KM	CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW	root development; ds.
XX	
OS	Nicotiana tabacum.
XX	
PN	WO9842851-A1.
XX	
PD	01-OCT-1998.
XX	
PF	24-MAR-1998; 98WO-EP01701.
XX	
PR	26-MAR-1997; 97EP-0302096.
XX	
PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX	
PI	Murray JAH;
XX	
DR	WPI; 1998-532012/45.
XX	
PT	Regulating growth and structure of plants by modulating protein that
PT	controls cell division - specifically a D-type cyclin, and related
PT	chimeric genes and transformed cells and plants, used to alter
PT	growth rate, flowering, seed production etc.
XX	
PS	Claim 14; p52-53; 75pp; English.
XX	
CC	This sequence represents the CYCD2;1 cDNA from Nicotiana tabacum which
CC	encodes a D-type cyclin. The sequence can be used to alter the growth
CC	characteristics or architecture of plants by altering the (functional)
CC	level in the plant cells of a cell-division controlling protein that can
CC	bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC	Modulation of the cyclin gene is used to increase or decrease the growth
CC	rate, provide faster germination, reduce time to flowering, increase the
CC	number of flowers, seeds or fruits per plant, increase root development,
CC	reduce height and to delay flowering in a range of plants, e.g. legumes,
CC	grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC	carnation, chrysanthemum, rose, tulip, etc.
XX	
SQ	Sequence 1284 BP; 415 A; 179 C; 261 G; 429 T; 0 other;

Query Match	5.28;	Score 116.8;	DB 19;	Length 1284;
Best Local Similarity	50.78;	Pred. No. 2.8e-19;		
Matches 280; Conservative	0;	Mismatches 272;	Indels 0;	Gaps 0;

[illegible]

Db	825	AAATCCCATCTCGGCCCTTGATTTCTGGATCATGCAACTGATATTAAAGCATATAAGAA	884
QY	822	AGGCTAGCTTCTTGCTTACTGGCCCTCATGCAATGCTGCTGCAGCCATACTACTGCAG	881
Db	885	GTAATTGATTTCTTGGCAATTCAGGCTCTTGAATAATTGCAGCATCAGTGGCAATGTCTGTTT	944
QY	882	CTAATGAAATTC	893
Db	945	CAGGGGAATAC	956

RESULT 10

ID AAZ94583 standard; DNA; 1173 BP.

... AAZ94583 ;
AC

DT 18-JUL-2000 (first entry)

DE Maize cyclin D ZmCYCD gene.

KW Maize; cyclin D; ZmCYCD gene; CYCD; cell division; cell cycle;

KW transgenic plant; ss.

05 Zea mays.

PN W0200017364-A2.

PD 30-MAR-2000.

21-SEP-1999; 99WO-US21946.

PR 23-SEP-1998; 98US-0101551.

PA (PION-) PIONEER HI-BRED INT INC.

PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;

PI Hoerster GJ;

DR WPI; 2000-283589/

XX

Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle

PT regulation

PS Claim 1; Page 122-124; 134pp; English.

The present sequence is that of an isoform of the maize ZmCycD gene that encodes cyclin D (CycD, see AA79323), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA294581-84) and polypeptides (see AA79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants,

PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.

PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 5.1%; Score 116; DB 21; Length 1356;
Best Local Similarity 52.5%; Pred. No. 4.6e-19;
Matches 254; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 405 GAGAGAATCAGTTGGATGGATTCTCAAGGTACACGGCTACTATGGCTTACGCCTTTGA 464
DB 366 GTGAAAAGGCTCTTGATGGATTTTAAAGTGAATCTCATTTATGCGTTTAATTCATTGA 425
QY 465 CGGCGTACCTCGCCGTCACTATATGATCGGTTTTTGATTCTCGCCGGTTGCCGAAA 524
DB 426 CGGCTCTTTAGCTGTTAATTACTTTCGATAGGTTTATTACAAGCAGGAAGTTTCAGACAG 485
QY 525 CAATGGGTGGCCTTCGCACTTGTATCTGTTCGATGCTTGTCTTTGGCAGCAAGATGG 584
DB 486 ATTAAGCATGGATGTCTCAGCTTACTGCTTGGCTGTCTGCTCTTTAGCTGTAAAGGTTG 545
QY 585 AAGAACCTCTTGGTTCATCTCTTGGACCTTCAGATAGAAGTGCCAAGTACATATTTG 644
DB 546 AAGAGATCCGTGTCTCTTTCTCTTAGATTTTCAAGTGAAGAGAAGCAAGATATGCTTTG 605
QY 645 AGCCGAGAACAAATTGATGAGATGAGCTACTTGTCTCGGTGTCTTAGATGAGGCTAA 704
DB 606 AAGCTAAGACTATACAGAGAATGAGCTTCTGTCTGTCTTACTCTTGTACTGTGAGGATGC 665
QY 705 GATCAGTAACCACTTTGCTTCCTCGCTTCTTTGGCGTCAAAAGTAGATTCAACTGGAA 764
DB 666 ATCCTGTGACTCCAATCTCGTTTTTGCATCAATTAATTCAGATACAGCTTAAATCTC 725
QY 765 CTTTATCCGGTTCCTTATTTCCAGGGGCAACAGAAATCATCGTATCTAATATCCAAGAG 824
DB 726 ATCATCAATTGAGTCTTGTAGTAGATGTAATCTTTATTACTCTCCATTAATTCCTGATT 785
QY 825 CTAGCTTCTGCTTACTGCGCTTCATGATGTGCTGCGACCATTAATCACTGACGCTA 884
DB 786 CGAGATTTCTGAGTTTTAGTCTCTGTGTAGCCACTGCAATATGGTCTGTATTATTA 845
QY 885 ATGA 888
II

Db 846 GAGA 849

RESULT 12
AAC33723
ID AAC33723 standard; DNA; 1358 BP.
XX
AC AAC33723;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 4087.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 22-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.

PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Db 488 ATAAGCATGGATGCTCTCAGCTTACTGCTTTGGCTGTGTCGTCTTAGCTGCTAAGGTTG 547

QY 585 AAGAACCTCTTGTTCCATCTCTCTTGACCTTCAGATAGAGGTGCCAAGTACATATTTG 644

Db 548 AAGAGATCCGTGTTCCCTTTCTCTTAGATTTTCAAGTGAAGAACGAATATGTCCTTG 607

QY 645 AGCCGAGAACAAATTCGTAGATGAGGTACTGTCTCGGTGCTTAGATTGAGGCTAA 704

Db 608 AAGCTAAGACATATACAGAGAATGAGCTTCTGTCTGCTACTCTTGACTGGAGATGC 667

QY 705 GATCAGTAAACACCACTTTGCTTCCTCGCTTCTTTGCGTGCAAGTAGATTCAACTGGAA 764

Db 668 ATCCTGTGACTCCAACTCTCGTTTTCGATCACAATTATTCGAGATACAGCTTAAATCTC 727

QY 765 CTTTATACCGGTTCCCTTATTTCCAGGGCAAGAAATCATGCTATCTAATATCCAGAGG 824

Db 728 ATCATCAATGGAGTCTCTTAGATAGATGGAATCTTATTACTCTCCATTATTCCTAAT 787

QY 825 CTAGCTTCTCTGCTTACTGGCCCTTCATGCAATTGCTGCTGACGCATTACTCACTGCAGTA 884

Db 788 CGAGATTCTGAGATTTTAGTCCCTCTGTGTTAGCCCACTGCAATATAGGTCTCTGTATTA 847

QY 885 ATGA 888

Db 848 GAGA 851

RESULT 13	
ID AAV33889	AAV33889 standard; cDNA to mRNA; 1846 BP.
XX	
AC AAV33889;	
XX	
DT 25-JAN-1999	, (first entry)
XX	
DE Maize CYCD2 gene.	
XX	
KW D-type cyclin; growth; plant; cell-division control; phosphorylation;	
KW CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;	
KW root development; ds.	
XX	
OS Zea mays.	
XX	
PN W09842851-A1.	
XX	
PD 01-OCT-1998.	
XX	
PF 24-MAR-1998;	98WO-EP01701.
XX	
PR 26-MAR-1997;	97EP-0302096.
XX	
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.	
XX	
PI Murray JAH;	
XX	
DR WPI; 1998-532012/45.	
XX	
PT Regulating growth and structure of plants by modulating protein that	
PT controls cell division - specifically a D-type cyclin, and related	
PT chimeric genes and transformed cells and plants, used to alter	
PT growth rate, flowering, seed production etc.	
XX	
PS Claim 14; p64-65; 75pp; English.	
XX	
CC This sequence represents the CYCD1.1 cDNA from Zea mays which encodes	
CC a D-type cyclin. The sequence can be used to alter the growth	
CC characteristics or architecture of plants by altering the (functional)	
CC level in the plant cells of a cell-division controlling protein that can	
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.	
CC Modulation of the cyclin gene is used to increase or decrease the growth	
CC rate, provide faster germination, reduce time to flowering, increase the	
CC number of flowers, seeds or fruits per plant, increase root development,	
CC	

OY	635	TACATATTGAGCCCGAACAATACTCGTAGGATGGAGCTACTTGTCTCGGGTGCTTAGAT	694
Db	809	TTTGTTTTTGAGGAAGCACCATAAAAAAGGATGGAGCTTCCTGGTGCTAAGCACCTTAAG	868
OY	695	TGAGGCTAAGATCAGTAACACCACTTGTGCTTCGCTTCTTGTGGCGTCAAGTAGAT	754
Db	869	TGGAGGATGCATGCTGTACTGCTTGTCTCATTTGTGAATACTTCTTCATAAATGAGT	928
OY	755	TCAACTGGAACCTTTAACCGGTCCTTATTTCCAGGGCAAGAATCATCGTATCTAAT	814
Db	929	GATCATGGTGCACCCCTCCTTGTCTTGACGCTCTCGCTTCGGACCTTGTCTTGAGCAC	988
OY	815	ATCCAAGAGGCTAGCTTCTTCTTACTTGCCCTTCATGCATTTGCTGTGAGGCCATACTC	874
Db	989	GCTAAAGGTGCTGAATTCGTGTATTTCAGACCCCTCCGAGATTGCTGCCAGTGTTCAC	1048
OY	875	ACTGC 879	
Db	1049	GCTGC 1053	

RESULT 15

AAZ94582

ID AAZ94582 standard; DNA; 1077 BP.

AC AAZ94582;

DT 18-JUL-2000 (first entry)

DE Malze cyclin D ZmCYCD gene.

KW Maize; cyclin D; ZmCYCD gene; CYCD: cell division; cell cycle; transgenic plant; SS.

05 Zea mays.

PN WO200017364-A2.

PD 30-MAR-2000.

21-SEP-1999; 99MO-US21946.

PR 23-SEP-1998; 9805-0101551.

AA
PA
(PION-) PIONEER HI-BRED INT INC.

AA
PI
Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA:

PI Hoerster GJ;

DR WPI; 2000-283589/24.

DR P-PSDB; AAY79322.

Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, PT related proteins and antisense RNA useful for control of cell cycle regulation -

PS Claim 1; page 120-121; 134pp; English.

The present sequence is that of an isoform of the maize ZmCycD gene that encodes cyclin D (CycD, see AAY793322), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AAZ94581-84) and polypeptides (see AAY79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and

growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polynucleotides can be used to identify CycD interacting proteins. All claimed.

Sequence 1077 BP; 228 A; 265 C; 308 G; 276 T; 0 other;

Query Match 4.98; Score 110.6; DB 21; Length 1077;

Best Local Similarity 51.88; Pred. No. 9.6e-18;

Matches	251;	Conservative	0;	Mismatches	234;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	------	--------	----	------	----

395 GCCAACGCCAGAGAAGATCAGTTGGATGGATTCTCAAGGTACACGCCGTACTATGGCTTT 454

Db 295 GTGCCGTCAGGAGGACGCCATCGATTGGATTGGAAGTCATTGAGCATTACAATTTC 354

455 CAGCCTTGACGGCGTACCTCGCCGTCACCTATATGATCGGTTTGGATTCTCGCCGG 514

Db 355 GCACCGTTGACTGCCGTTTGTCTGTGAACCTACCTCGATAGATTCCCTCCACGATGAG 414

515 TTGCCGGAACAATGGGTGGCCTCTGCACTTGTATCTGTTGCATGCTTGTCTTTGGCA 574

Db 415 TTCCCTGAAGCAGAGCTTGATGACTCAGCTCTGGCAGTGGCTTGTCTTGGCT 474

QY 575 GCAAGATGGAAGACCTCTTGTCCATCTCTTGGACCTCAGATAGAAGTGCCAAG 634

Db 475 TCGAAATCGAAGAGACTTTTGTGCCACTCCCCCTGGATTTCAGGTAGCGGAGCAAG 534

635 TACATATTGAGCCGAGACAATTCGTAGGATGGAGCTACTTGTTCGCTTAGAT 694

Db 535 TTTGTTTTTGAGGGAAGCATTAAAAAGCATGGAGCTTCTGGTCTAAGCACCTTAAG 594

695 TGGAGGCTAAGATCAGTAACACCACCTTTGCTTCCTCGCTTTCCTTGGCGTGCAAGTAGAT 754

Db 595 TGGAGGATGCATGCTGTTACTGCTTGCCTCATTTGTGAACTTCTTCATAAATTGAGT 654

QY 755 TCAACTGGAACCTTTATCCGGTTCCTTATTTCCAGGGCAACAGAATCATCGTATCTAAT 814

Db 655 GATCATGGTGCACCCCTCCTTGCTTGCACGCTCTCGCTCTCGGACCTTGTCTTGAGCACC 714

815 ATCCAGAGGCTAGCTTCTTGCTTACTGGCCTTCATGCATTGCTGCTGCAGCCATCTC 874

Db 715 GCTAAGGTGCTGAATTCGTGATTCAGACCCCTCCGAGATTGCTGCCAGTTGCACCTT 774

QY 875 ACTGC 879

Db 775 GCTGC 779

Search completed: October 25, 2002, 23:40:58
Job time : 372 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 22:41:35 ; Search time 2663 Seconds
(without alignments)
11449.351 Million cell updates/sec

Title: US-09-665-308D-11
Perfect score: 2259
Sequence: 1 acaactctccaccatc.....ttaaaaaaaaaaaaaa 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.8	23.3	548	10	BI427409 sah79h05.
2	518	22.9	560	10	BI785106 sal37a11.
3	508.6	22.5	809	10	BG585146 EST486909
4	492.2	21.8	834	10	BG585934 EST487699
5	489.4	21.7	810	10	BG646052 EST507671
6	483.4	21.4	775	10	BG645553 EST507172
7	450.8	20.0	663	10	BI270081 NF004A12F
8	429.4	19.0	480	10	BG238202 sab63e07.
9	408.2	18.1	533	10	BG238135 sab62f07.
10	406.8	18.0	718	10	BG647122 EST508741
11	382.8	16.9	749	10	BG886881 EST512732
12	337.2	14.9	621	10	BI432702 EST535463
13	329	14.6	558	10	BF520221 EST457690
14	310.6	13.7	716	10	BG526521 60-9 Stev
15	287	12.7	728	10	BG597062 EST495740
16	229.8	10.2	313	10	BF008678 ss68e07.y
17	215	9.5	651	9	AW776661 EST335726

18	211.2	9.3	658	9	AW981189	AW981189 EST392383
19	205.6	9.1	501	10	BI436332	BI436332 EST539093
20	169.8	7.5	585	10	BG595067	BG595067 EST493745
21	169.6	7.5	515	10	BE323695	BE323695 NF005D03P
22	166	7.3	287	10	BE801432	BE801432 srl4e07.y
23	149	6.6	197	10	BF636916	BF636916 NF073G01L
24	145.6	6.4	557	10	BM309337	BM309337 sak57d12.
25	142	6.3	583	9	AI812774	AI812774 18H7 plne
26	141	6.2	813	10	BE642779	BE642779 Cr12_6_P2
27	134.4	5.9	546	9	AW944884	AW944884 EST336934
28	132.8	5.9	478	10	BE472260	BE472260 EST417113
29	129.4	5.7	596	9	AW042725	AW042725 ST24F07 P
30	129.2	5.7	659	10	BM358501	BM358501 GA_Ea001
31	127.2	5.6	523	10	BE472243	BE472243 EST417096
32	126.6	5.6	731	10	BM408328	BM408328 EST582655
33	126.6	5.6	802	10	BI207010	BI207010 EST525050
34	125	5.5	666	10	BI210187	BI210187 EST528227
35	118	5.2	621	10	BE442681	BE442681 WHE1101_A
36	113.6	5.0	485	10	BG132909	BG132909 EST465801
37	113.2	5.0	790	10	BI306295	BI306295 NL_4_B12
38	112.2	5.0	558	9	AW036252	AW036252 EST278331
39	109	4.8	608	9	AW735876	AW735876 EST336644
40	108.8	4.8	478	9	AV527915	AV527915 AV527915
41	107	4.7	516	10	BI211043	BI211043 EST529083
42	105.4	4.7	546	10	BI204893	BI204893 EST522933
43	105.4	4.7	725	10	BI203937	BI203937 EST521977
44	105.4	4.7	727	10	BI204715	BI204715 EST522755
45	105.4	4.7	727	10	BI205090	BI205090 EST523130

ALIGNMENTS

RESULT 1
BI427409
LOCUS
DEFINITION sah79h05.y1 Gm-c1049 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1049-4594 5', mRNA sequence.
ACCESSION BI427409 GI:15204641
VERSION
KEYWORDS
SOURCE
ORGANISM
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE
1 (bases 1 to 548)
Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
location/Qualifiers
1..548
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1049-4594"
/clone_11b="Gm-c1049"

/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the Bluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."

BASE COUNT 167 a 70 c 150 g 161 t
ORIGIN

Query Match 23.3%; Score 525.8; DB 10; Length 548;
Best Local Similarity 98.5%; Pred. NO. 4.5e-75;
Matches 541; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 1424 TGCAGAAATTCACCTAGGAGAGGAGATTTCGCACATGTTACCGTGGAGAGAAATGAG 1483
|||||
Db 1 TGCAGAAATTCACCTAGGAGAGGAGATTTCGCACATGTTACCGTGGAGAGAAATGAG 60

QY 1484 AGAAGAAAGAAAGTGAACACTGAACCCAGGGGTAGAAGATTTAATGTGATTGTTCTGT 1543
|||||
Db 61 AGAAGAAAGAAAGTGAACACTGAACACAGGGGTAGAAGATTTAATGTGATTGTTCTGT 120

QY 1544 AACCTGTGATTCTGAAGAGAAAGATTGAGTTGGCGGCTGGAATTTCAAAGTTGCATTAA 1603
|||||
Db 121 AACCTGTGAGTGTGAAGAAAGAGTGAAGTTGGCGGCTGGAATTTCAAAGTTGCATTAA 180

QY 1604 TACTTGGTGAAGAGATGAAGATGCTGGGGGCAACGCTGTAGAGATTGAGAAAGAA 1663
|||
Db 181 TA-TTGTGAAGAGATGAAGATGCTGGGGGCAACGCTGTAGAGATTGAGAAAGAA 239

QY 1664 AAGTAGAGAGAAAGTATGAAAACTCTGCTGATTATTTGAAGTTGAAACTTAGAAGTTTG 1723
|||||
Db 240 AAGTAGAGAGAAAGTATGAAAACTCTGCTGATTATTTGAAGTTGAAACTTAGAAGTTTG 299

QY 1724 AAGTGTCAATGTTCAATATCATGCTAATTAAGTCAAGCAAGCTTCATTCTTGCCCA 1783
|||||
Db 300 AAGTGTCAATGTTCAATATCATGCTAATTAAGTCAAGCAAGCTTCATTCTTGCCCA 359

QY 1784 GCATCACTGCTTCTTCATCATCCACGTTACTACTTTGATGGGACCCCTCAACAGTAAA 1843
|||||
Db 360 GCATCACTGCTTCTTCATCATCCACGTTACTACTTTGATGGGACCCCTCAACAGTAAA 419

QY 1844 GAACAATTTGAAGGGCAATAAGTTGAGTTGGCTACAATCGTGACTTTTTTGTGGG 1903
|||||
Db 420 GAACAATTTGAAGGGCAATAAGTTGAGTTGGCTACAATCGTGACTTTTTTGTGGG 479

QY 1904 TATTGGCACGCTGCAGTCGGTCTGGGCTGCCAATGAAGTGTGACGTGATTTT 1963
|||||
Db 480 TATTGGCACGCTGCAGTCGGTCTGGGCTGCCAATGAAGTGTGACGTGATTTT 539

QY 1964 CTTTTCCTT 1972
|||||
Db 540 CTTTTCCTT 548

RESULT 2
LOCUS BI785106 560 bp mRNA linear EST 30-NOV-2001
DEFINITION sai37a11.y1 Gm-cl065 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl065-5397 5', similar to SW:CGD1_ARATH P42751 CYCLIN
DELTA-1. ;, mRNA sequence.
ACCESSION BI785106

VERSION BI785106.1 GI:15812831
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 560)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritters,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
TITLE JOURNAL
COMMENT Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 422.

FEATURES
source
1..560
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-5397"
/clone_lib="Gm-cl065"
/tissue_type="germinating shoots"
/lab_host="DH10B"

/note="Vector: Bluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the Bluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."

BASE COUNT 108 a 180 c 137 g 135 t
ORIGIN

Query Match 22.9%; Score 518; DB 10; Length 560;
Best Local Similarity 96.3%; Pred. NO. 8e-74;
Matches 543; Conservative 0; Mismatches 15; Indels 6; Gaps 1;

QY 26 CAACCACACACACTCTCTCTCCCTCTCTGACCAAAACCACTTCTCCGGGACATCTCC 85
|||
Db 3 CATCAACAACCACTCTCTCTCCCTCTCTGACCAAAACCAATTTCTCCGGGACATCTCC 62

QY 86 GGTACAGTTCGGGCAACCTCATCGGCGAATCGCATGCCAACACATGAATCGGAACCT 145
|||||
Db 63 GTTCAGTTCGGGCAAGCTCTCCGGGACATCGGCAATCAATGAATCGGAATC- 121

QY 146 CCGCTGCCCGCGCGCTCTCATGTGCTTCTGCTCTCCGACTACGACCTCTCTGCG 205
|||||
Db 122 -----ACCGCGGGGCTCTCATGTGCTTCTGCTCTCCGACTACGACCTCTCTGCG 176

QY 206 GCGGAGGACTCTCTCCGGAATCTCTCCGGAGAGTTCGCGGAGTGTCTCTTCCGACATC 265
|||||
Db 177 GCGGAGGACTCTCTCCGGAATCTCTCCGGAGAGTTCGCGGAGTGTCTCTTCTCCGACATC 236

QY 266 GACTCTCTACCTCTCCGCCGTCGCGACAGAGATTGTATTGATCGCGAGCTTC 325
|||||
Db 237 GACTCTCTACCTCTCCGCCGTCGCGACAGAGATTGTATTGATCGCGAGCTTC 296

QY 326 ATCGACACGAGCGCAACTTCGTCGCGGATTCGAGTACTGTCCGGTTCCAAATCTCC 385
|||||
Db 297 ATCGACACGAGCGCAACTTCGTCGCGGATTCGAGTACTGTCCGGTTCCAAATCTCC 356

QY 386 TCCCTGACGCGCAACGCGCAGAGAATCAGTTGGATGATCTCAAGTACACGCGTAC 445
|||||
Db 357 TCCCTGACGCGCAACGCGCAGAGAATCAGTTGGATGATCTCAAGTACACGCGTAC 416

QY 446 TATGGCTTTCAGCCTTTGACGGGTACCTCGCCGTCACTATATGATCGCTTTTGAT 505
|||||
Db 417 TATGGCTTTCAGCCTTTGACGGGTACCTCGCCGTCACTATATGATCGCTTTTGAT 476

QY 506 TCTCGCGGTTGCGCGGAACAATGGGTGGCTCTGCACTTGTATCTGTTCATGCTTG 565
|||||
Db 477 TCTCGCGGTTGCGCGGAACAATGGGTGGCTCTGCACTTGTATCTGTTCATGCTTG 536

QY 566 TCTTTGGCAGCAAGATGAGAA 589
|||||
Db 537 TCTTTGGCAGCAAGATGAGAA 560

RESULT 3
BG585146 809 bp mRNA linear EST 11-APR-2001
LOCUS
DEFINITION EST486909 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone PMHAM-22A23 5' end, mRNA sequence.
ACCESSION BG585146
VERSION BG585146.1 GI:13600210
KEYWORDS
SOURCE
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE
AUTHORS 1 (bases 1 to 809)
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Utterback,T., Cho,J.
and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula after colonization with
Glomus versiforme, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N380619e TIGR sequence name: MTDCA12TK More
information is available at: http://www.medicago.org
Seq primer: Skmod (CTA gAA CTA gTg gAT CC).
location/Qualifiers
1. 809
/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="PMHAM-22A23"
/clone_lib="MHAM"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0R"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
stratagene and packaged using gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised

FEATURES
Source

from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0R cells.
BASE COUNT 194 a 196 c 173 g 246 t
ORIGIN

Query Match 22.5%; Score 508.6; DB 10; Length 809;
Best Local Similarity 78.7%; Pred. No. 2.3e-72;
Matches 637; Conservative 0; Mismatches 159; Indels 13; Gaps 2;

QY 158 GCGCTCTCATGTGCGTTTCCTGCTCTCCGACTACGACCTCTCTCGCGGAGACTCC 217
|||
Db 1 GCAATCTCATGCGCACTGTCCAGACCTCCGACTCGGAGCTCTCTCGCGGAGACTCG 60

QY 218 TCCGGAATCCTCTCCGAGAGATCGCCGGAGTGTCTTCTCCGACATCGACTCTCACC 277
|||
Db 61 TCGGAGGTCTCTACCGGAGATTTACCGGAATGCTCTCCGACCTGATTCATCATCA 120

QY 278 CCTCCGCGTCCGCGACACA-----GAGGATGTTATTGATCGCGAGCTTC 325
|||
Db 121 TCGCAGTTGCCGTGCTGCTCATTTATTTGCCGAGAGAGAGAGAGATGCTGTTTC 180

QY 326 ATCGACACGAGCGCAACTTCGTTCCGGGATTCGAGTACCTGTCCGGTTCCAAATCTCC 385
|||||
Db 181 ATCGACACGAGTTCAAGTTGTCTCTGTTTCGACTACGCTCTCAAGATTCCAATCTCC 240

QY 386 TCCCTGACGCCAAGCCAGAGAAGAAATCAGTTGATGATTTCTCAAGTACACGCGTAC 445
|||||
Db 241 TCTCTGCAATCCAGACACAGAGAAGAACCAATGATGATTTCTCAAGTACATGAGTAT 300

QY 446 TATGGCTTTCAGCCTTTGACGGCGTACCTCGCGTCACTATATGATGATGCTTTTGAT 505
|||||
Db 301 TATGGATTTTCAGCGCTTAACGGCGTACCTCTCCGTTAACTATATGATGATGCTTTTGAT 360

QY 506 TCTCGCGGTTGCCGGAACAATGGGTGGCTCTGCACTTGTATCTGTTCATGCTTG 565
|||||
Db 361 TCTCGACCTTTACCGGAATCAATGATGATGCGCCACTGCACTTTATCTGTTCATGCTTG 420

QY 566 TCTTTGGCAGCAAGATGGAAGAACCTCTGTTCCATCTCTCTTGACCTTCAGATGAA 625
|||||
Db 421 TCTTTAGCAGCAAGATGGAAGAACCACTGTTCTCTCTCTTAGACTTCAGATTGAA 480

QY 626 GTGCCAAGTACATATTGAGCCGAGAACAAATTCGTAGATGAGTACTGTTCTCGGT 685
|||||
Db 481 GTGCCAATACATATTTCACCAAGACGATCTTAGAATGAGCTGTTGTTCTGACT 540

QY 686 GTCTTAGATTGAGGCTAAGATCAGTAACACCACTTTGCTTCTCGCTTTCTTGCGTGC 745
|||
Db 541 ATTTTGATTTGAGGCTGAGATCAATCAACCCCACTAGTTTCTCAAGTTCTTTGCGTGC 600

QY 746 AAAGTAGATTCAACTGGAAGCTTTTATCCGGTCTCTATTTCAGGGCAGACAGAAATCATC 805
|||
Db 601 AAGCTAGATTCAACTGGAAGCTTTTCAACCACTTCATTAATTCACGTGCTACAGAAATCATC 660

QY 806 GTATCTAATATCCAAAGAGCTAGCTTTCTGTTACTTGCCCTTCATGCTGCTGCA 865
|||||
Db 661 TTATCTAATATCCAAAGAGCTAGCTTTCTTACTTACAGGCCATCATGCTGCAAGCT 720

QY 866 GCCATACTCACTGCACTAATGAATTCCTAATTTGCTGTGTTAAGCCGAAATGCT 925
|||||
Db 721 GCCATACTCTCTGCACTAATGAATTCCTAATTTGCTGTGTTAATTCCTGAGCATGCT 780

QY 926 GAGTCAT-GGTGCGAGGACTAAGAAAG 953
|||
Db 781 GAATCATGGGTGTAAGACTAAGCAAG 809

RESULT 4
BG585934 834 bp mRNA linear EST 11-APR-2001
LOCUS
DEFINITION EST487699 MHAM Medicago truncatula/Glomus versiforme mixed EST
library cDNA clone PMHAM-31L19 5' end, mRNA sequence.
ACCESSION BG585934
VERSION BG585934.1 GI:13600998

ACCESSION DELTA-1. ; mRNA sequence.
VERSION BG238202 GI:12773275
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 480)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 445.
Location/Qualifiers
1..480
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl043-4046"
/clone_lib="Gm-cl043"
/tissue_type="Hypocotyl and plumule, germinating seeds"
/lab_host="DH10B"
/note="Vector: pT7T3Pac (Pharmacia); Site_1: EcoRI;
Site_2: NotI; This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestion with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the pT7T3-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.
Randy Shoemaker."
BASE COUNT 89 a 164 c 112 g 115 t
ORIGIN
Query Match 19.0%; Score 429.4; DB 10; Length 480;
Best Local Similarity 95.4%; Pred. No. 1.5e-59;
Matches 455; Conservative 0; Mismatches 16; Indels 6; Gaps 1;
QY 26 CAACACACACTCTCTCTCCCTCTCTGACCAAAACCACTTCTCCGGCAGCATCTCC 85
DB 10 CATCAACAACACTCTCTCTCCCTCTCTGACCAAAACCAATTCTCCGGCAGCATCTCC 69
QY 86 GGTACAGTTCGGCAACCTCATCGCGCAATCGCATGCAACACAATGAATGCGAATCT 145
DB 70 GGTACAGTTCGGCAGCTCTCCGGCAGCTCGCATGCAACTCAATGAATGCGAATC- 128
QY 146 CCGCTGCGCGCGGCTCTCATGTCGGTTTCTGCTGCTTCGCACTACGACCTCTCTGC 205
DB 129 -----ACGCGCGGGGCTCTCATGTCGGTTTCTGCTGCTTCGCACTACGACCTCTCTGC 183
QY 206 GCGAGACTCTCTCCGAATCTCTCCGAGAGATCGCCGAGTGTCTCTCTCCGACATC 265
DB 184 GCGGAGACTCTCTCCGAATCTCTCTCCGAGAGATCGCCGAGTGTCTCTCTCCGACATC 243

QY 266 GACTCTACCTCTCTCCCGCCGTCGCCGACGACAGAGATTGTATTTCATCCGAGCTTC 325
DB 244 GACTCTACCTCTCTCCCGCCGTCGCCGACGACGACAGAGATTGTATTTCATCCGAGCTTC 303
QY 326 ATCGAGCAGAGCGCACTTCTGTTCCGGGATTCGAGTACTGTGCGCGTTCCAACTCTCGC 385
DB 304 ATCGAGCATGAGCGCACTTCTGTTCCGGGATTCGAGTACTGTGCGCGTTCCAACTCTCGC 363
QY 386 TCCCTGACGCCCAACGCCAGAGAAGATCATGTCGATTCTCAAGCTACACGCGTAC 445
DB 364 TCCCTGACGCCCAACGCCAGAGAAGATCATGTCGATTCTCAAGCTACACGCGTAC 423
QY 446 TATGGCTTTCAGCCTTTGACGGCGGTACTCGCCGTCACATATATGATCGGTTTGTG 502
DB 424 TATGGCTTTCAGCCTTTGACGGCGGTACTCGCCGTCACATATATGATCGGTTTGTG 480
RESULT 9
LOCUS BG238135
DEFINITION 533 bp mRNA linear EST 28-NOV-2001
sab62f07.y1 Gm-cl043 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-cl043-4093 5' similar to SW:CGD1_ARATH P42751 CYCLIN
DELTA-1. ; mRNA sequence.
ACCESSION BG238135
VERSION BG238135.1 GI:12773208
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 533)
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
Location/Qualifiers
1..533
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl043-4093"
/clone_lib="Gm-cl043"
/tissue_type="Hypocotyl and plumule, germinating seeds"
/lab_host="DH10B"
/note="Vector: pT7T3Pac (Pharmacia); Site_1: EcoRI;
Site_2: NotI; This cDNA library was constructed from mRNA
isolated from hypocotyl and plumule tissues of seeds
germinated for three days of the cultivar Williams.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a NotI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by digestion with EcoRI and NotI. The
cDNA fragments were directionally cloned into the
EcoRI-NotI restriction site of the pT7T3-Pac vector. The
ligated cDNA fragments were transformed into DH10B host
cells (Gibco BRL). This library was constructed by Dr.

	Db	655	CTATATGTTGTATGTA	670	
	RESULT 11				
	LOCUS	BG886881			
	DEFINITION	BG886881	EST512732 cSTD Solanum tuberosum cdna clone cSTD214 5' sequence,	749 bp mRNA linear EST 30-MAY-2001	
	ACCESSION	BG886881			
	VERSION	BG886881.1	GI:14263967		
	KEYWORDS	EST.			
	SOURCE	potato.			
	ORGANISM	Solanum tuberosum			
	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	TITLE	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.			
	JOURNAL	1 (bases 1 to 749)			
	COMMENT	van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,T., Chiemiango,A.; Bougrl,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from dormant potato tubers Unpublished (2001) Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seq primer: M13F-R.			
	FEATURES				
	source	Location/Qualifiers			
		1..749			
		/organism="Solanum tuberosum"			
		/cultivar="Kennebec"			
		/db_xref="taxon:4113"			
		/clone="cSTD214"			
		/clone_lib="cSTD"			
		/tissue_type="dormant tuber"			
		/dev_stage="one month post-harvest"			
		/lab_host="SOLR"			
		/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."			
	BASE COUNT	197 a 181 c 146 g 225 t			
	ORIGIN				
	Query Match	16.9%; Score 382.8; DB 10; length 749;			
	Best Local Similarity	70.3%; Pred. No. 4e-52;			
	Matches 529; Conservative	0; Mismatches 217; Indels	6; Gaps	1;	
OY	374	TTCCAATCTCGTCCCTGGAGCCCAACGCCAGAGAATCATCTGGATGATTCTCAAG	433		
Db	4	TTCCAATCTCAATCTCTAAGCGCCGCCGCTAGAGATGAATCCGTTGCATGATTCTCAAG	63		
OY	434	GTAACACGGCTACTATGGCTTCAGCCCTTGACGGCGTACCTGCCGTCACATATATGGAT	493		
Db	64	GTAACAAGCCACTATAGGTTCCAGCCCAATTAAGCGCGTATCTGCCGTTAACTATTTGAT	123		
OY	494	CGGTTTTTGGATTCTCGCCGCTGCGGGAACAATAATGGTGCCCTGCAACTGTATCT	553		
Db	124	CGTTTTCTCTACTCGAAGAGCTTGCCGCAACAATAATGGTGCCCACTTCAACTATTTGCG	183		
OY	554	GTTGCATGCTGTCTTGTGGCAGCAAAAGATGGAAGAACCTCTGTCCATCTCTCTTGAC	613		
Db	184	GTTGCTTGTCTTATCTTAGCACAAAATGAGGAACCTCTGTCTTCCCTTTTGAT	243		
OY	614	CTTCAGATAGAAGGTGCCAAGTACATATTTGAGCCGAGAACAAATTCGTAGATGAGCTA	673		
Db	244	CTTCAGGTGAAGGCGCAAAGTATATATTGAACCBAAAACTATCCAAAGATGAGTTT	303		
OY	674	CTTGCTCTCGGTCTCTTAGATTGAGAGGCTAAGATCAGTAACACCACTTTGCTTCTCGCT	733		

[illegible]

infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from *Phytophthora* rather than potato."

Query Match	14.98;	Score 337.2;	DB 10;	Length 621;
Best Local Similarity	74.18;	Pred. No. 9.2e-45;		
Matches 440; Conservative	0;	Mismatches 153;	Indels 1;	Gaps 1;

QY 307 TTATTCGATCGCGAGCTTCAATCGACGACGAGCGCAACTTCGTCCGGGATTGAGTACCCT 366
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 26 TGAATCAATCGCGGTTCTTAATCGAAAGATGAACGMAATTTTGTAACCTGGATTGACTATAT 85

QY 367 GTCCGCGTTCCAATCTCGCTCCTCGACGCCAACGCCAGAGAANAATCAGTTGGATGGAT 426
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 CGAGAAATTCCAATCTCAATCTCTAAGCGCCGCCGCTAGAGATGAATCCGTTGCATGGAT 145

QY 427 TCTCAAGGTACACGCGTACTATGGCTTTACGCCCTTGACGGCGTACTCGCCGCTCAACTA 486
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 146 TCTCAAGGTACACAACGCCACTATAGGTTTTCCAGCCATTAAAGCGCGTATCTCGCCGTTAACTA 205

QY 487 TATGATCGGTTTTTGGATTCTCGCCGGTTGCCGGAACAAATGGGTGGCTCTGCAACT 546
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 206 TTTCGATCGTTTTCTCTACTCGAAGAACTTGCCGCAACAAATGGCTGGCCACTTCAACT 265

QY 547 TGTATCTGTGCATGCTGTCTTTGGCAGCAAAGATGGAAGAACCTCTTGTTCCATCTCT 606
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 266 ATTGTCGGTGTGCTTGCGTATCTTAGCTGCAAAATGGAAGAACCTCTTGTTCCCTCTCT 325

QY 607 CTTCGACCTTCAGATAGAGGTGCCAAGTACATATTTGAGCCGAGAACAAATTCGTAGGAT 666
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 326 TTTCGATCTTCAGGTTGAAGCGGCAAAAGTATATATTGAACCAAAAACTATCCAAAAGAAAT 385

QY 667 GGAGCTACTTGTCTCTCGGTCTTAGATTGGAGGCTAAGATCAGTAACCACTTTGCTT 726
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 386 GGAATTTCTGTGTGAGGATATTAGATTGGAGGCTCCGATCATTAACCTCCGTTAGCTT 445

QY 727 CCTCGCTTTCTTTGGCGTGAAGTAGATTCAACTGGAACCTTATCCGGTTCCTTATTTTC 786
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 446 CCTCAGTTCTTTGGCGGCTAAACTGTGATTCACCTAGGAACCTTCACCTGCGTTCCTTATATC 505

QY 787 CAGGGCAACAGAATAATCATCTATCTAATATATCCAAGAGGCTAGC-TTCTTGCTTACTGGC 845
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 506 AAGGGCTTCTCAGATTATCTCTCTAATATTCAAGAAAGCTTAGCTTTTCATGAGTATTTGGC 565

QY 846 CTTCATGATTTGCTGCTGACGCCATCTCACTGCAGCTAATGAATTCCTAATT 899
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 566 CATCATGATAGCTGACGATCAATACTATATGTGACAGCTAAGAGCCTTCCAAATT 619

RESULT 13	
BF520221	
LOCUS	558 bp mRNA linear EST 08-DEC-2000
DEFINITION	EST457690 DSIL Medicago truncatula cDNA clone pDSIL-22P18, mRNA sequence.
ACCESSION	BF520221
VERSION	BF520221.1 GI:11608904
KEYWORDS	EST.
SOURCE	barrel medic.
ORGANISM	Medicago truncatula
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE	1 (bases 1 to 558)
AUTHORS	Fedorova,M., Plereson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
TITLE	ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii
JOURNAL	Unpublished (2000)

COMMENT

Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
University of Minnesota name: M277659e
TIGR sequence name: MTFCP93TK
More information is available at: <http://chrysie.tamu.edu/medicago>
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

FEATURES

```

/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIL-22P18"
/clone_lib="DSIL"
/tissue_type="leaves infected with colletotrichum
trifolii"
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells. Note: EST may
be of fungal origin."

```

Query Match	14.6%	Score 329	DB 10	Length 558
Best Local Similarity	78.2%	Pred. No. 2e-43		
Matches 440	Conservative 0	Mismatches 105	Indels 18	Gaps 3
QY 716	CCACCTTTGGCTTCCTCGCTTTCTTTGGCGTGC	AAAGTAGATTC	CACTGGAACTTTTATCCGG	775
Db 2	CCACTTAGTCTCCTCCTCAGTTTCTTTGGCGTGC	AAAGTAGATTC	CACTGGAACTTTTACCCCTC	61
QY 776	TTCCCTTATTTCCAGGGCAAGAAATCATCGTATC	TAATATCCAAAGAGCTAGCTTTCTT		835
Db 62	TTCATATATTTACAGTGCCTACAGAAATCATCTT	ATATATCCAAAGATGCTAGCTTTCTT		121
QY 836	GCTTACTGGCCTTCATGCATTTGCTGCTGCAGCC	ATACCTCAGCTATGAAATTTCT		895
Db 122	ACTTACAGGCCCATCATGCATTTGCTGCAGCTGC	CCATACCTCTCTGCAGCTAATGAAATTTCT		181
QY 896	AATTTGCTCTGTGTTAAGCCCGAAATGCTGAGTC	ATGTTGTCGAGGGACTAAGAAAGAA		955
Db 182	AATTTGCTCTTTGTTAATCCTGAGCATGCTGAAT	CATGTTGTGTAAGGACTAAGCAAAAGAA		241
QY 956	AAAGTAATAGGCTGCTACCAAGTTGATGCAAGAG	CTTGTGATTAACAATTAACCAACGGAAA		1015
Db 242	AAATATATAGGCTGCTATGATTCAGAAATTTGT	AGTACGCAATTAACCAAGAAAT		301
QY 1016	CTCCCTTACTAAAAAGTGTTCGCCGACGCTGCAG	AGTAACACTCGGACCCGAATGAGTCA		1075
Db 302	GCCCC-----TAAAGTGTTCACACAGTTGCGAG	TTACAGCTCGGACCGAAGAGGTGTTCC		355
QY 1076	AGTA-----CTGTATCATCATTTCTCATCATCC	CTTTCAACCTCCTTCTCCTTGTCT		1126
Db 356	ACTGTCTCGTGTGCTCATCATCTCCATCTTCCCT	CTTCAACCTCCTTCTTGTGTCT		415
QY 1127	TGTAAGAGGAGGAAATTAATAACCGTTTGTGGGT	AGAA--TGACAAAGGAAACTCCGAG		1183
Db 416	TATTAAGAGGAAATTAATAGCTGTTCTGGGTAGAT	GTGACAAAGGAAACTCAGAG		475
QY 1184	TGAAGAGAAAAAGAACAACTAATTAATAAAGAA	GGGAAAGGAAAGAGGGAATTAAGGTGG		1243

||||| 476 TGAAGAGAAAAAGAACAAACAGAAATATTAATAAGAGAACAGAGAAATAAGGTGG 535
QY 1244 GCCAAGTTGCTAGAAACCTCA 1266
Db 536 GCCAGGTGCTAGAAACCTCA 558
RESULT 14
LOCUS BG526521 716 bp mRNA linear EST 16-NOV-2001
DEFINITION 60-9 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
sequence.
ACCESSION BG526521 GI:16950010
VERSION BG526521.1
KEYWORDS EST.
SOURCE Stevia rebaudiana.
ORGANISM Stevia rebaudiana.
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Asteridae; euasterids II; Asterales; Asteraceae; Asteroidae;
Heliantheae; Stevia.
1 (bases 1 to 716)
Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P.
Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
diterpene synthesis
Unpublished (2001)
CONTACT: Jim Brandle
JOURNAL Genomics and Biotechnology
COMMENT Agriculture and Agri-Food Canada - SCPPRC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandleje@em.agr.ca
Seq primer: T3 promoter primer.
LOCATION/Qualifiers
FEATURES
source 1. .716
/organism="Stevia rebaudiana"
/strain="751/1501"
/cultivar="Landrace"
/db_xref="taxon:55670"
/clone_lib="Stevia field grown leaf cDNA"
/issue_type="leaf"
/dev_stage="field grown, mid-size"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from field grown leaves. Mid-size actively growing leaves
were collected and pooled from several plants and frozen
immediately after harvesting in liquid nitrogen. The cDNA
was prepared using an XhoI-poly(dT) linker-primer. An
EcoRI adapter was ligated to the blunt-end cDNA and the
products were digested with EcoRI and XhoI enabling
directional cloning into the lambda ZAP Express vector.
The library was amplified using the host strain XL1-Blue
MRF'. Mass excision of the library was performed to
obtain pBK-CMV phagemid clones in the host strain XL0LR.
Single pass DNA sequencing was performed using the T3
promoter primer: 5' ATTAACCTCCTCACTAAAGGA 3'. This library
was constructed by Alex Richman."
BASE COUNT 186 a 154 c 157 g 202 t 17 others
ORIGIN
Query Match 13.7%; Score 310.6; DB 10; Length 716;
Best Local Similarity 69.2%; Pred. No. 1.7e-40;
Matches 454; Conservative 0; Mismatches 199; Indels 3; Gaps 3;

Db 69 TCGNGCATCTGCTAGAGAAATCGGTTGCCCTGGATCCCTTAAGGNCACAGCTTTTACG 128
QY 450 GCTTTCAGCCTTTGACGGCGGTACCTCGCCGCTCACTATATGATCGGTTTGGATTCTC 509
Db 129 GNTTCAACCATGACGGCGGTACCTTCCTGCTCACTACCTGGATCGTTTCATCTATGNC 188
QY 510 GCCGGTTGCCGGAACAATGAGGCTGCTGCAACTGTATCTGTTCATGCTGTCTT 569
Db 189 GCGGCTTCCCGGTGGCAACGCGGTGCGCTTGCACCTTTATCTGNTGCATGCTGNCCT 248
QY 570 TGGCAGCAAGATGGAAGAACCTCTGTTCCATCTCTCTTGGACCTTCAGATAGAAGTGC 629
Db 249 TAGCTGCTAAATGAGAGAAACCATTAATCTTCAATCTTGATCTTCAGGTTGAAGGNC 308
QY 630 CCAAGTACATATTGAGCCGAGAACAAATTCGTAGATGAGCTACTGTCTCGTCT 689
Db 309 CAAATATATCTTTGAAACCTAAACACATCCAAAGATGAGGTTCTTGNACTTGGTGT 368
QY 690 TAGATTGAGGCTAAGATCAGTAAACACCTTTCCTTCCTTCTTTCGCTGCAAG 749
Db 369 TGGATTGAGACTACGATCCGTTACACCGTTTACGCTTATCGGATATTTTTCGATAGA 428
QY 750 TAGATTCACTGGAACCTTTATCCGGTCTTATTTCCAGGGGCAAGAAATCATCGTAT 809
Db 429 TCGATCCATCTGGAATGTATACGGGATTCCTTATCTCAAGGGCGCAAAATATCTAT 488
QY 810 CTAATATCCAAGAGCTAGCTTTCTTCTTACTGCGCTTCATGCAATGCTGTCAGCCA 869
Db 489 CAATATATCAAGAGCTAGTTACTTGAGTATGGCATCATGATGATGCAAGTCAACCA 548
QY 870 TACTCAGTCGACCTAATGAATTCCTAATTTGGTCTGTGGTTAAGCCCGAAATGCTGAT 929
Db 549 TACT-TTGGCAGCAAGNGATCTTTCTAATTTCTCACTCATCATATGCCG-ACATGCCGAT 606
QY 930 CATGTCGAGGAGCACTAAGAAAAGAAAGTATAGGGTGCTACCACTGATGCAA 985
Db 607 CATGGGGNGATGGGCTCAACAAAGAGAGATTCNNAATGTTCCAGATTANNCAA 662
RESULT 15
LOCUS BG597062 728 bp mRNA linear EST 12-APR-2001
DEFINITION EST495740 cSTS solanum tuberosum cDNA clone cSTS16p1 5' sequence,
mRNA sequence.
ACCESSION BG597062
VERSION BG597062.1 GI:13615202
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 728)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generations of ESTs from sprouting potato eyes
Unpublished (2000)
JOURNAL Contact: Cathy Ronning
COMMENT The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: M13F-R.
FEATURES
source 1. .728
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone_lib="cSTS16p1"
/clone_lib="cSTS"
/issue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."

BASE COUNT 183 a 178 c 144 g 223 t
ORIGIN

Query Match 12.7%; Score 287; DB 10; Length 728;

Best Local Similarity 68.1%; Pred. No. 1e-36;

Matches 430; Conservative 0; Mismatches 195; Indels 6; Gaps 2;

```
QY 175 TTCCCTGCTCTCCGACTACGACCTCCTCTGCGGAGAGACTCCTCCGAACTCTCTCCGG 234
    ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 TTACTCCGACTGCTTCTCCGACTACTCTGCGGCGAAGACTCC---GATACCGTTTCT 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 235 AGAGTCGCCGAGTGCTCTCTCCGACATCGACTCCTCACCCTCTCCGCCGCGGAC 294
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 150 CAAACGAGAGAGAGAGATTGGCCGGAAT--GTTCCTCGTCGATATCGAATCTCAGTT 207
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 295 GACAGAGAGATTGTTATTCGATCCGAGCTTCATCGAGACAGCGCAACTTCGTTCCGG 354
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 208 CGCCGATATCGATGAATCAATCGCGGCTTATCGAAGATGACGAATTTGTTACCTGG 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 355 ATTCGAGTACCTGTGCGGTTCCAACTCGCTCCCTGACGCCCAAGCCAGAGAAGATC 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 268 ATTTGACTATATCGAAGAAATTCGAATCTCAATCTTAAGCGCGCGCTAGAGATGAATC 327
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 415 AGTTGATGATTTCTCAGGTACACGCCGTACTATGGCTTCAGCCTTTGACGGCGTACCT 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 328 CGTTGCATGGATTCTCAAGGTACACGCCCACTATGGTTTCCAGCCATTAACGGCGTATCT 387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 475 CGCCGTCACATATATGATCGGTTTGGATTCTCGCCGGTGGCCGGAACAATGGGTG 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 388 CGCCGTTAACTATTTCGATCGTTTCTTCTACTCGAAGACTTGCCGCAACAATGGCTG 447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 535 GCCTGTGCACTGTATCTGTTCAGTGTCTGCTTTGGCAGCAAAAGATGGAACCTCT 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 448 GCCACTTCACTATATGTCGGTTCGCTGCTATCTTTAGCTGCAAAAATGAGAACCTCT 507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 595 TGTTCATCTCTTGGACCTTCAGATAGAGGTGCCAAGTACATATTGAGCCGAGAAC 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 508 TGTTCCTTCTTTTGGATCTTCAGGTTGAGGTGCCAAGTATATATTGAAACCAAAAC 567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 655 AATTGATGAGAGCTACTGTCTCGGTCTTCTTGTAGATTGAGGCTAAGATCAGTAAC 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 568 TATCCAAAGAAATGAGATTCTTGTGCTGAGGATATTAGATTGAGGCTCCGATCCATAAC 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 715 ACCACTTGTCTCTCGCTTCTTGTGCGTGAAGTAGATTCAACTGGAACCTTTATCCG 774
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 628 TCCGTTAGCTTCTCAGCTTCTTTCAGCTTAACCTGATTCACTAGGAACCTTCACTGCG 687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 775 GTTCCTTATTTCAGGGCAACAGAATCATC 805
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 688 TTTCCTTATCTCAAGGCTTCTCAGATTATC 718
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: October 26, 2002, 00:25:39
Job time : 2672 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 23:28:24 ; Search time 71 Seconds
(without alignments)
7815.297 Million cell updates/sec

Title: US-09-665-308D-11
Perfect score: 2259
Sequence: 1 acaacttcctccactcatc.....ttaaaaaaaaaaaaaaaaaa 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/1na/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/1na/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	66	2.9	7218	1 US-08-232-463-14	Sequence 14, Appl
2	53.4	2.4	7218	1 US-08-232-463-14	Sequence 14, Appl
3	45.4	2.0	2417	1 US-08-011-398B-1	Sequence 1, Appl
4	45.4	2.0	2417	1 US-08-464-051-1	Sequence 1, Appl
5	45.4	2.0	2417	2 US-08-462-498-1	Sequence 1, Appl
6	45.4	2.0	2417	3 US-08-554-385-2	Sequence 2, Appl
7	44.2	2.0	2417	1 US-08-011-398B-1	Sequence 1, Appl
8	44.2	2.0	2417	1 US-08-464-051-1	Sequence 1, Appl
9	44.2	2.0	2417	2 US-08-462-498-1	Sequence 1, Appl
c 10	44.2	2.0	2417	3 US-08-554-385-2	Sequence 2, Appl
11	43.2	1.9	246240	2 US-08-724-394A-20	Sequence 20, Appl
12	43.2	1.9	246240	2 US-08-724-394A-21	Sequence 21, Appl
13	43.2	1.9	246240	2 US-08-724-394A-22	Sequence 22, Appl
14	42.2	1.9	1215	2 US-09-092-770-8	Sequence 8, Appl
15	42.2	1.9	1215	4 US-09-222-851-8	Sequence 8, Appl
c 16	41	1.8	1798	2 US-08-557-128-12	Sequence 12, Appl
17	39.8	1.8	549	1 US-07-991-867B-28	Sequence 28, Appl
18	39.8	1.8	549	1 US-08-107-755A-28	Sequence 28, Appl
19	39.8	1.8	549	2 US-08-544-332-28	Sequence 28, Appl
20	39.8	1.8	1511	1 US-07-991-867B-8	Sequence 8, Appl
21	39.8	1.8	1511	1 US-08-107-755A-8	Sequence 8, Appl
22	39.8	1.8	1511	2 US-08-544-332-8	Sequence 8, Appl
23	39.8	1.8	4810	3 US-08-852-629-11	Sequence 11, Appl
24	39.8	1.8	4838	3 US-08-852-629-15	Sequence 15, Appl
25	39	1.7	1212	2 US-09-092-770-18	Sequence 18, Appl
26	39	1.7	1212	4 US-09-222-851-18	Sequence 18, Appl
c 27	38.8	1.7	669	1 US-08-463-115-17	Sequence 17, Appl

c 28	38.8	1.7	669	1 US-08-465-388-17	Sequence 17, Appl
c 29	38.6	1.7	388	2 US-08-623-906A-13	Sequence 13, Appl
c 30	38.4	1.7	296	1 US-08-738-367-8	Sequence 8, Appl
c 31	38.2	1.7	1730	1 US-07-817-920-1	Sequence 1, Appl
c 32	38.2	1.7	1730	1 US-08-117-006-1	Sequence 1, Appl
c 33	38.2	1.7	1730	1 US-08-216-594-1	Sequence 1, Appl
c 34	38.2	1.7	1730	5 PCT-US93-00149-1	Sequence 1, Appl
c 35	38	1.7	1079	1 US-07-781-355-1	Sequence 1, Appl
c 36	37.8	1.7	3380	2 US-09-156-425-1	Sequence 1, Appl
c 37	37.6	1.7	593	4 US-09-385-982-262	Sequence 262, App
c 38	37.4	1.7	817	4 US-08-885-469-1	Sequence 1, Appl
c 39	37.4	1.7	1554	2 US-08-031-538-8	Sequence 8, Appl
c 40	37.4	1.7	1889	3 US-09-187-050-1	Sequence 1, Appl
c 41	37	1.6	289	4 US-09-007-005-17	Sequence 17, Appl
c 42	37	1.6	289	4 US-09-244-796-17	Sequence 17, Appl
c 43	37	1.6	2862	4 US-08-569-749-13	Sequence 13, Appl
c 44	37	1.6	2862	5 PCT-US96-12860-13	Sequence 13, Appl
c 45	37	1.6	6124	4 US-08-213-419B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT2gpt-Fls
; US-08-232-463-14
Query Match 2.9%; Score 66; DB 1; Length 7218;

Best Local Similarity 3.8%; Pred. No. 7.9e-08;
Matches 15; Conservative 230; Mismatches 145; Indels 0; Gaps 0;

```
OY 1133 AGGAGGAATTAATAACCGTTGTGGTAGTACAAAGAACTCCAGTGAAGAGAA 1192
      || || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1464 AGTAGTTAAAGAGATAGAAGATTTGTACRRRRRRRRRRRRRRRRRRRRRRRR 1405

OY 1193 AACGAACAACAATATAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1252
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1404 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1345

OY 1253 TCTAGAACCTCAACATTTTGTAGAGGTTTTCATTAATAAATGACTGTGAGG 1312
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1344 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1265

OY 1313 TGTAGATTATAATAGTATATATGATATATCTATCGTATATACTAGAGAGTTGAT 1372
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1284 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1225

OY 1373 GGGTTGAGTAATTTTATTTTATGTTGCTGACTTATTAATATGAGTTTGCAGATT 1432
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1224 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1165

OY 1433 CACCTAGGAGGAGGATTTTGCACATGTTACCGTGGAGAGGAGGAGGAGGAG 1492
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1164 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1105

OY 1493 AAGTGAACACTGAACGAGGAGTAGAGAA 1522
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1104 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1075
```

RESULT 2

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTZgpt-Fls
US-08-232-463-14

Query Match 2.4%; Score 53.4; DB 1; Length 7218;
Best Local Similarity 2.4%; Pred. No. 0.0002;
Matches 9; Conservative 223; Mismatches 149; Indels 0; Gaps 0;

```
OY 3 AACTTCCTCCACTCATTCATCAACAACACACACACTCTCTCCCTCTGACCAAA 62
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1065 ATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1124

OY 63 ACCACTCTCCGCGACATCTCCGCTCAGTTCGCGCAACTCATCGGGAATCGGCATG 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1125 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1184

OY 123 CCAACAATGAATGCGGAACCTCCGCTGCCCGCGGCTCTCATGTGCTTCTGCC 182
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1185 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1244

OY 183 TCTCCGACTACGACCTCTCTGCGCGGAGGAGACTCTCCGGAATCTCTCCGAGAGTCCG 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1245 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1304

OY 243 CGAGTCTCTCTCTCCGACATCGACTCTCCTCCTCCGCGCTCCGCGAGAGAGG 302
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1305 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1364

OY 303 ATGTTATTCGATCGGAGCTTCATCGACAGCAGCGCAACTTGTCCGGATTGAGT 362
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1365 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1424

OY 363 ACCGTGCGGCTTCCAATCTC 383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1425 YYYYYYYYYYGTACCAAAATTC 1445
```

RESULT 3

US-08-011-398B-1

; Sequence 1, Application US/08011398B

; Patent No. 5512473

; GENERAL INFORMATION:

; APPLICANT: Roger Brent

; APPLICANT: Antonis S. Zervos

; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: Wordperfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/011,398B

; FILING DATE: 29 JAN 1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul T. Clark

; REGISTRATION NUMBER: 30,162


```
; GENERAL INFORMATION:
; APPLICANT: Roger Brent
; APPLICANT: Antonis S. Zervos
; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,385
; FILING DATE: NO. 6017692ember 8, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Karen F. Lech
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/252001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2417
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-554-385-2

Query Match          2.0%; Score 45.4; DB 3; Length 2417;
Best Local Similarity 63.1%; Pred. No. 0.016;
Matches 70; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 2147 CCTCTTTTCACATAGGGCTAAAGGCTTTGGGCTTTTCCGTGCTGCTGATTTGG 2206
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2307 CCTCTCCCTTACCTGGGAAGGCTCTTGAGACCTTACCCCTGGCTGTTGGACTTTG 2366
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 2207 ATTGATTATATATATGACACTATTATTCTTAAAAA 2257
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2367 TATACTTTAATAATTAATTAACCTTAATTACTTAAAAA 2417
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
US-08-011-398B-1/c
; Sequence 1, Application US/08011398B
; Patent No. 5512473
; GENERAL INFORMATION:
; APPLICANT: Roger Brent
; APPLICANT: Antonis S. Zervos
; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
```

```
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/011,398B
; FILING DATE: 29 JAN 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/160001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2417
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-011-398B-1

Query Match          2.0%; Score 44.2; DB 1; Length 2417;
Best Local Similarity 66.0%; Pred. No. 0.034;
Matches 64; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2163 GGTAAAGTCTTTGGGCTTTTCCGTGCTGCTGATTTGATTTGATTAATAATAA 2222
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 GGAAGGCTCTTGAGACCTTACCCCTGGCTGTTGGACTTTGTATTAATAAT 103
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 2223 TGACACTATTATTCTTAAAAA 2259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 102 TACTACCTTAATTACTTAAAAA 66
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-464-051-1/c
; Sequence 1, Application US/08464051
; Patent No. 5780262
; GENERAL INFORMATION:
; APPLICANT: Roger Brent
; APPLICANT: Antonis S. Zervos
; TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,051
; FILING DATE: 05 JUN 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,398
; FILING DATE: 29 JAN 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/160002
; TELECOMMUNICATION INFORMATION:
```



```

; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
;
US-08-724-394A-20
```

```

Query Match      1.9%; Score 43.2; DB 2; Length 246240;
Best Local Similarity 45.2%; Pred. No. 0.71;
Matches 159; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1274 TAGAGGGTTTGGCAATTAATAATGACTGTGAGGCGGTGAGATTATATAGTATATA 1333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27153 TAAATTAATTGAATTATTTTAAATACTACTACCTAAATTCCTAAATTAATTAATAATTA 27212

QY 1334 TATGATATATCTCTATCGTATATACTAAGAGAGTTGATGGGTTGGAGTAATTTTATT 1393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27213 TATTACCTGAATATTACTTAAATAATAGATTTTTAAATAAATAAATAAATAAATAA 27272

QY 1394 TTTATGTTGGTGAATTATTAATATGAGTTTGCAGAAATTCACCTAGGGAAGGAGATT 1453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27273 ATAGATTTTAAATAAATAAATAAATAATGAATGAAGCCCTAAATATCTGGCATCAT 27332

QY 1454 GCGACATGTTACCGTGGGAGAGAAATGAGAGAAGAAAGAGTGAACACTGAACAGG 1513
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27333 GCTATTAAGTAGAGAGCCCAAGAAATATATAATATTTTACCACACTCAAAAAAAC 27392

QY 1514 GTAGAAGAATTAAATGATGTTGTTCTGTAACTGTGATCTCTGAAGGAAGAATTGAGT 1573
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27393 TATTAATTAATACAAAGGTATATGATTCATGTGAGAAATCAAGATTTGAGGATGAACATTAAT 27452

QY 1574 TGGGGGCTGATTTCAAGTTTGCATTAATTACTTGGTGAAGGAGATGAAG 1625
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27453 AAAACAGAGACTTTGAGAGAGAAATAATTAATTGGGAAAGGTCCAGAAAG 27504
```

```

RESULT 12
US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
;
US-08-724-394A-21
```

```

Query Match      1.9%; Score 43.2; DB 2; Length 246240;
Best Local Similarity 45.2%; Pred. No. 0.71;
Matches 159; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1274 TAGAGGGTTTGGCAATTAATAATGACTGTGAGGCGGTGAGATTATATAGTATATA 1333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27153 TAAATTAATTGAATTATTTTAAATACTACTACCTAAATTCCTAAATTAATTAATAATTA 27212

QY 1334 TATGATATATCTCTATCGTATATACTAAGAGAGTTGATGGGTTGGAGTAATTTTATT 1393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27213 TATTACCTGAATATTACTTAAATAATAGATTTTTAAATAAATAAATAAATAAATAA 27272

QY 1394 TTTATGTTGGTGAATTATTAATATGAGTTTGCAGAAATTCACCTAGGGAAGGAGATT 1453
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27273 ATAGATTTTAAATAAATAAATAAATAATGAATGAAGCCCTAAATATCTGGCATCAT 27332

QY 1454 GCGACATGTTACCGTGGGAGAGAAATGAGAGAAGAAAGAGTGAACACTGAACAGG 1513
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27333 GCTATTAAGTAGAGAGCCCAAGAAATATATAATATTTTACCACACTCAAAAAAAC 27392

QY 1514 GTAGAAGAATTAAATGATGTTGTTCTGTAACTGTGATCTCTGAAGGAAGAATTGAGT 1573
```


Db 27393 TATTAATACAGGCTATGATTCATGTCAGATCAAGATTGAGATGACATAAT 27452
QY 1574 TCGGGGCTGATTCAAGCTTGCATTACTTGGTGAAGAGATGAAG 1625
Db 27453 AAAACAGAGACTTTGAGAGAGAAAATAATATTGGAGAGTCCAGAAAG 27504

RESULT 13
US-08-724-394A-22

; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Laufer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereeto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Flits, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match 1.9%; Score 43.2; DB 2; Length 246240;
Best Local Similarity 45.2%; Pred. No. 0.71;
Matches 159; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1274 TAGAGGCTTTTGCATTAAATAAGCTTGAGTGAGGCTAGATTATATAGATATA 1333
Db 27153 TAAATAATTGCAATATTATAAATACTACCTAAATTCCTAATAATTACATAAATTA 27212
QY 1334 TATGATATATCTCTATCGTATATACCTAAGAGAGTTTGATGGGTTTGAGTAAATTTTAAAT 1393
Db 27213 TATTACCTGATATTTACCTAAATAATAATAGATTTTAAATAATAATAATAATAATAATAA 27272
QY 1394 TTTATGTTGGTGAAGCTTATTAATATGAGTTTGCAAGATTCACCTAGGGAAGAGGATTTT 1453

Db 27273 ATAGATTTTAAATAATAATAATAATAATGCAATAAGCCCCCTAAATATCTGCAATCAT 27332
QY 1454 GCGACATGTTACCGTGGAGAGAAATGAGAGAAAGAAAGTGAACACTGAACACAGG 1513
Db 27333 GCTATAAGTAGAGAGAGCCAAAGCAATATAATAATATGAATATTTTACCACCTCAAAAAAAC 27392
QY 1514 GTAGAGAAATTTAATGTGATTTGTTCTTGTACCTGTGATTCGAAGAAAGAAATTTAGT 1573
Db 27393 TATAAATAATACAGGCTATATGATTCATGTCAGATCAAGATTTTGAGGATGAACATAAT 27452
QY 1574 TCGGGGCTGATTCAAGCTTGCATTACTTGGTGAAGAGATGAAG 1625
Db 27453 AAAACAGAGACTTTGAGAGAGAGAAAATAATATTGGGAAGGTCCAGAAAG 27504

RESULT 14
US-09-092-770-8

; Sequence 8, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119e1 Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092,770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human
US-09-092-770-8

Query Match 1.9%; Score 42.2; DB 2; Length 1215;
Best Local Similarity 28.2%; Pred. No. 0.084;
Matches 131; Conservative 82; Mismatches 243; Indels 9; Gaps 2;

QY 275 CCTCTCGCGCCGCGCCGACAGACAGAGATTGTTATTCGATCGGAGCTTCATCGAGCAC 334
Db 295 CCNWSNCCNYTNCNGAYTTNWSNTGGGNTGWSNARGARGTNGYTNAAYATGYTN 354
QY 335 GAGCGCACTTCGTTCCGGGATTCGAGTACCTGTCGGGTTCCAACTCCGCTCCGTTGAC 394
Db 355 AARAARGARWSNMGNTAYGTNCAYGAYARCAATTTYGARGTNTNCAYWSNGAYTTNGAR 414
QY 395 GCCAAGCCAGAGAAATCAGTTGATGATCTCAAGGTACACGCGTACTATGGCTTT 454
Db 415 CCNCARATGMNSNATHYNTNGAYTGGYNTNGARGTNTGARGTNTAYACNYTN 474
QY 455 CAGCCTTTGACGGCGTACCTCGCCGTCACATATATGATCGGTTTGGATTCTCGCCG 514
Db 475 CAYMGNGARACNTTYTAYTTNGCNCARGAYTTTYGAYMGNTTYATGYTNACNC----- 529
QY 515 TTGCCGGAACAATGGGTGGCCCTGCAACTGTATCTGTGCAATGCTTGTCTTGGCA 574
Db 530 -AARAAGAYATHAAYARAAYATGYTNCARATNATHGNATHACWSNNTNTTYATHGCN 588
QY 575 GCAAGATGGAAGAACCTCTGTTCCATCTCTTGACCTTCAGATGAGAAGGTGCAAG 634
Db 589 WSNABRYTNGARGARATHTAYGCNCCNABRYTNCARGARTTYGC--NTAYGTNACNGAY 645
QY 635 TACATATTTGAGCCGAGAACAAATTCGTAGAGATGAGACTACTGTCTCCGCTGTAGAT 694
Db 646 GGNGCNTGYWSNGARGARGAYATHTYTNMGNTGARGRTNATHATHTNAARGCNYTNAAR 705
QY 695 TGGAGGCTAAGATCACTAACAACCACTTTCCTCTCTCTCTT 739
Db 706 TGGGARTTNTGTCGCTNACNATHATHTMSNTGTYTNAAYTTNTTY 750

RESULT 15

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:34:14 : Search time 34 Seconds
(without alignments)
1107.471 Million cell updates/sec

Title: US-09-665-308D-12
Perfect score: 1758
Sequence: 1 MSVSCLSDYDLLCGEDSSGI.....SCKRRKLNRLMYDDKGNSE 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
7:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
8:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
9:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*
10:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*
12:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*
13:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
14:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22:	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1758	100.0	339	AAV31894	Soybean cyclin del
2	1262	71.8	318	AAV31895	Soybean cyclin del
3	1030	58.6	328	AAV29789	Arabidopsis thalia
4	1030	58.6	339	AAV29788	Arabidopsis thalia
5	1011	57.5	320	AAV29790	Arabidopsis thalia
6	502.5	28.6	358	AAV79321	Maize cyclin D. Z
7	496.5	28.2	358	AAV79322	Maize cyclin D. Z
8	470	26.7	390	AAV79323	Maize cyclin D. Z
9	467	26.6	388	AAV31897	Gorn cyclin delta-
10	420.5	23.9	308	AAV47103	Arabidopsis thalia
11	419.5	23.9	307	AAV23947	Arabidopsis thalia

12	419.5	23.9	367	21	AAV23946	Arabidopsis thalia
13	418.5	23.8	308	21	AAV23337	Arabidopsis thalia
14	411	23.4	361	21	AAV07075	Arabidopsis thalia
15	411	23.4	361	21	AAV33864	Arabidopsis thalia
16	410.5	23.4	308	20	AAV14071	Mitogenic cyclin C
17	406	23.1	287	21	AAV47104	Arabidopsis thalia
18	404	23.0	287	21	AAV23338	Arabidopsis thalia
19	402.5	22.9	273	21	AAV47105	Arabidopsis thalia
20	400.5	22.8	273	21	AAV23339	Arabidopsis thalia
21	396.5	22.6	308	21	AAV07076	Arabidopsis thalia
22	396.5	22.6	308	21	AAV33865	Arabidopsis thalia
23	340	19.3	349	21	AAV79324	Maize cyclin D. Z
24	318.5	18.1	238	20	AAV31892	Corn cyclin delta-
25	305.5	17.4	262	21	AAV50160	Arabidopsis thalia
26	305.5	17.4	373	21	AAV50154	Arabidopsis thalia
27	305	17.3	240	21	AAV23948	Arabidopsis thalia
28	295	16.8	263	21	AAV20271	Arabidopsis thalia
29	272.5	15.5	232	21	AAV07077	Arabidopsis thalia
30	272.5	15.5	232	21	AAV53866	Arabidopsis thalia
31	267.5	15.2	181	20	AAV31893	Arabidopsis thalia
32	255	14.5	318	20	AAV31900	Rice cyclin delta-
33	251	14.3	341	21	AAV08430	Corn cyclin delta-
34	250.5	14.2	307	21	AAV08431	Arabidopsis thalia
35	247.5	14.1	298	21	AAV08432	Arabidopsis thalia
36	221	12.6	509	21	AAV35800	Protein involved 1
37	199.5	11.3	424	21	AAV35801	Protein involved 1
38	197	11.2	420	21	AAV43702	Human cancer assoc
39	196	11.1	398	20	AAV87566	A cyclin related p
40	196	11.1	398	22	AAV92927	Human protein sequ
41	194.5	11.1	146	21	AAV20272	Arabidopsis thalia
42	194.5	11.1	146	21	AAV50161	Arabidopsis thalia
43	194.5	11.1	257	21	AAV50155	Arabidopsis thalia
44	194	11.0	481	22	AAV64233	Drosophila melanog
45	184.5	10.5	421	22	AAV09366	Novel human diagno

ALIGNMENTS

RESULT 1	
AAV31894	
ID	AAV31894 standard; Protein; 339 AA.
AC	AAV31894;
XX	
DT	21-DEC-1999 (first entry)
XX	
DE	Soybean cyclin delta-1.
XX	
KW	Cyclin delta-1; soybean; cell cycle; cell division;
KW	transgenic plant; herbicide; plant breeding.
XX	
OS	Glycine max.
XX	
PN	WO9948486-A2.
XX	
PD	30-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06047.
XX	
PR	23-MAR-1998; 98US-0078948.
XX	
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	
PI	Cahoon RE, Klein TW, Odell JT, Orozco EM;
XX	
DR	WPI; 1999-591036/50.
DR	N-PSDB; AAZ19958.
XX	
PT	New isolated plant cyclin genes, used to develop products for use as
PT	herbicides and for developing plant breeding programs -
XX	
PS	Claim 6; Page 52-53; 68pp; English.

XX This is the deduced amino acid sequence of a corn cyclin delta-1
CC protein derived from the nucleotide sequence (see AA219958) of a
CC contig composed of clones isolated from soybean Authority (TM)
CC herbicide-sprayed and soybean root ear cDNA libraries. It
CC represents the entire protein. The invention relates to isolated
CC nucleic acid fragments (see AA219953-66) encoding cyclin A, cyclin
CC delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see
CC AA21889-902). It also relates to the construction of chimeric genes
CC encoding all or a portion of a cyclin, in sense or antisense
CC orientation, where expression of the chimeric gene results in altered
CC levels of the cyclin protein in a transformed host cell. This would
CC have the effect of altering the regulation of cell division in those
CC cells. The nucleic acid fragments may be used to express cyclins in
CC plant cells to enhance cell tissue culture growth. The availability
CC of nucleic acid sequences encoding all or a portion of cyclins should
CC facilitate studies of cell cycle in plants, provide genetic tools
CC to enhance cell growth in tissue culture, increase the efficiency
CC of gene transfer and help provide more stable transformations. The
CC proteins can be used as targets to facilitate design and/or
CC identification of inhibitors of those enzymes that may be useful as
CC herbicides.

XX Sequence 339 AA;

Query Match 100.0%; Score 1758; DB 20; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.6e-185;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVSCLSYDYLGGEDSSGILSGESPECSFSDIDSSPPPTTEDCYSTASFIHERNF 60
Db 1 MSVSCLSYDYLGGEDSSGILSGESPECSFSDIDSSPPPTTEDCYSTASFIHERNF 60
QY 61 VPGFEYLSRFQSRSDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPET 120
Db 61 VPGFEYLSRFQSRSDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPET 120
QY 121 NGWPLQLVSVACLSIAAKMEPLVPSLDDIQIEGAKYIFEPRTIRRMELVLGVLDWRLR 180
Db 121 NGWPLQLVSVACLSIAAKMEPLVPSLDDIQIEGAKYIFEPRTIRRMELVLGVLDWRLR 180
QY 181 SVTPLCLFAFACKVDSTGTFRILISRATEIIVSNIQEASFAYWPSCIAAAAILTAAN 240
Db 181 SVTPLCLFAFACKVDSTGTFRILISRATEIIVSNIQEASFAYWPSCIAAAAILTAAN 240
QY 241 EIPNWSVVKPENAESWEGLRKEKVIQCYQLMQLVYINNQRKLPPLKVLPLQRLVTTTR 300
Db 241 EIPNWSVVKPENAESWEGLRKEKVIQCYQLMQLVYINNQRKLPPLKVLPLQRLVTTTR 300
QY 301 MRSSTVSSFSSTSTFSLSCKRRKLNRLWVDDKGNSE 339
Db 301 MRSSTVSSFSSTSTFSLSCKRRKLNRLWVDDKGNSE 339

RESULT 2
AA21895
ID AA21895 standard; Protein; 318 AA.

XX AA21895;
AC
XX 21-DEC-1999 (first entry)
DT
XX
DE Soybean cyclin delta-1 partial polypeptide.
XX
KW Cyclin delta-1; soybean; cell cycle; cell division;
transgenic plant; herbicide; plant breeding.
XX
OS Glycine max.
XX
PN WO948486-A2.
XX
PD 30-SEP-1999.
XX

PF 19-MAR-1999; 99WO-US06047.
XX
PR 23-MAR-1998; 98US-0078948.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Klein TM, Odell JT, Orozco EM;
XX
DR WPI; 1999-591036/50.
XX
DR N-PSDB; AA219959.

PT New isolated plant cyclin genes, used to develop products for use as
PT herbicides and for developing plant breeding programs -
XX
PS Claim 6; Page 54-55; 68pp; English.

XX This is the deduced amino acid sequence of a corn cyclin delta-1
CC protein derived from the nucleotide sequence (see AA219959) of a
CC clone isolated from a soybean embryo cDNA library. It represents
CC 95% of the entire protein. The invention relates to isolated
CC nucleic acid fragments (see AA219953-66) encoding cyclin A, cyclin
CC delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see
CC AA21889-902). It also relates to the construction of chimeric genes
CC encoding all or a portion of a cyclin, in sense or antisense
CC orientation, where expression of the chimeric gene results in altered
CC levels of the cyclin protein in a transformed host cell. This would
CC have the effect of altering the regulation of cell division in those
CC cells. The nucleic acid fragments may be used to express cyclins in
CC plant cells to enhance cell tissue culture growth. The availability
CC of nucleic acid sequences encoding all or a portion of cyclins should
CC facilitate studies of cell cycle in plants, provide genetic tools
CC to enhance cell growth in tissue culture, increase the efficiency
CC of gene transfer and help provide more stable transformations. The
CC proteins can be used as targets to facilitate design and/or
CC identification of inhibitors of those enzymes that may be useful as
CC herbicides.

SQ Sequence 318 AA;

Query Match 71.8%; Score 1262; DB 20; Length 318;
Best Local Similarity 78.2%; Pred. No. 3.2e-130;
Matches 255; Conservative 29; Mismatches 28; Indels 14; Gaps 7;

QY 18 SGIISGESPECSFSDIDSSPPPTTEDCYSTASFIHERNFVPGFEYLSRFQSRSDA 77
Db 3 AGIND-SSPECS-SDIDSSPP-----SEASIIAGFMEDEENFVPGFEYLSRFQSRSDA 54
QY 78 NAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRL-PETNGWPLQLVSVACLSIA 136
Db 55 SAREESVAVILKVQAYYAFQPYTAYLSVNYLDRLNSRPLPKTNGWPLQLVSVACLSIA 114
QY 137 AKMEPLVPSLDDIQIEGAKYIFEPRTIRRMELVLGVLDWRLRSVTPLCLFAFACKVD 196
Db 115 AKMESLVPPLDDIQIEGAKYIFEPRTIRRMELVLGVLDWRLRSVTPLCLFAFACKVD 174
QY 197 STGTFRILISRATEIIVSNIQEASFAYWPSCIAAAAILTAANEIPNWSVVKPENAESW 256
Db 175 STGTFRILISRATEIIVSNIQEASFAYWPSCIAAAAILTAANEIPNWSVVKPENAESW 234
QY 257 CEGLRKEKVIQCYQLMQLVYINNQRKLPPLKVLPLQRLVTTTRMRSSTVSSF--SSSSS 314
Db 235 CEGLRKEKVIQCYQLMQLVYINNQRKLP--KVLPLQRLVTTTRMRSSTVSSFSSSSSP 292
QY 315 TSFSLCKRRKLNRLWV-DDKGNSE 339
Db 293 SSSSLCKRRKLNRLWVDDKGNSE 318

RESULT 3
AAG29789
ID AAG29789 standard; Protein; 328 AA.
XX
AC AAG29789;

XX	17-OCT-2000	(first entry)	
XX	Arabidopsis thaliana	protein fragment SEQ ID NO: 35502	
DE			
XX			
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128234.	
PR	08-APR-1999;	99US-0128714.	
PR	16-APR-1999;	99US-0129845.	
PR	19-APR-1999;	99US-0130077.	
PR	21-APR-1999;	99US-0130449.	
PR	23-APR-1999;	99US-0130510.	
PR	23-APR-1999;	99US-0130891.	
PR	28-APR-1999;	99US-0131449.	
PR	30-APR-1999;	99US-0132048.	
PR	30-APR-1999;	99US-0132407.	
PR	04-MAY-1999;	99US-0132484.	
PR	05-MAY-1999;	99US-0132485.	
PR	06-MAY-1999;	99US-0132486.	
PR	06-MAY-1999;	99US-0132487.	
PR	07-MAY-1999;	99US-0132863.	
PR	11-MAY-1999;	99US-0134256.	
PR	14-MAY-1999;	99US-0134218.	
PR	14-MAY-1999;	99US-0134219.	
PR	14-MAY-1999;	99US-0134221.	
PR	14-MAY-1999;	99US-0134370.	
PR	18-MAY-1999;	99US-0134768.	
PR	19-MAY-1999;	99US-0134941.	
PR	20-MAY-1999;	99US-0135124.	
PR	21-MAY-1999;	99US-0135353.	
PR	24-MAY-1999;	99US-0135629.	
PR	25-MAY-1999;	99US-0136021.	
PR	27-MAY-1999;	99US-0136392.	
PR	28-MAY-1999;	99US-0136782.	
PR	01-JUN-1999;	99US-0137222.	
PR	03-JUN-1999;	99US-0137528.	
PR	04-JUN-1999;	99US-0137502.	
PR	07-JUN-1999;	99US-0137724.	
PR	08-JUN-1999;	99US-0138094.	
PR	10-JUN-1999;	99US-0138540.	
PR	10-JUN-1999;	99US-0138847.	
PR	14-JUN-1999;	99US-0139119.	
PR	16-JUN-1999;	99US-0139452.	
PR	16-JUN-1999;	99US-0139453.	
PR	17-JUN-1999;	99US-0139492.	
PR	18-JUN-1999;	99US-0139454.	
PR	18-JUN-1999;	99US-0139455.	
PR	18-JUN-1999;	99US-0139456.	
PR	18-JUN-1999;	99US-0139457.	
PR	18-JUN-1999;	99US-0139458.	
PR	18-JUN-1999;	99US-0139459.	
PR	18-JUN-1999;	99US-0139460.	
PR	18-JUN-1999;	99US-0139461.	
PR	18-JUN-1999;	99US-0139462.	
PR	18-JUN-1999;	99US-0139463.	
PR	18-JUN-1999;	99US-0139750.	
PR	18-JUN-1999;	99US-0139763.	
PR	21-JUN-1999;	99US-0139817.	
PR	22-JUN-1999;	99US-0139899.	
PR	23-JUN-1999;	99US-0140353.	
PR	23-JUN-1999;	99US-0140354.	
PR	24-JUN-1999;	99US-0140695.	
PR	28-JUN-1999;	99US-0140823.	
PR	29-JUN-1999;	99US-0140991.	
PR	30-JUN-1999;	99US-0141287.	
PR	01-JUL-1999;	99US-0141842.	
PR	02-JUL-1999;	99US-0142154.	
PR	06-JUL-1999;	99US-0142055.	
PR	08-JUL-1999;	99US-0142390.	
PR	09-JUL-1999;	99US-0142803.	
PR	12-JUL-1999;	99US-0142977.	
PR	13-JUL-1999;	99US-0143542.	
PR	14-JUL-1999;	99US-0143624.	
PR	15-JUL-1999;	99US-0144005.	
PR	16-JUL-1999;	99US-0144085.	
PR	16-JUL-1999;	99US-0144086.	
PR	19-JUL-1999;	99US-0144325.	
PR	19-JUL-1999;	99US-0144331.	
PR	19-JUL-1999;	99US-0144332.	
PR	19-JUL-1999;	99US-0144333.	
PR	19-JUL-1999;	99US-0144334.	
PR	19-JUL-1999;	99US-0144335.	
PR	20-JUL-1999;	99US-0144352.	
PR	20-JUL-1999;	99US-0144632.	
PR	20-JUL-1999;	99US-0144884.	
PR	21-JUL-1999;	99US-0144814.	
PR	21-JUL-1999;	99US-0145086.	
PR	21-JUL-1999;	99US-0145088.	
PR	22-JUL-1999;	99US-0145085.	
PR	22-JUL-1999;	99US-0145087.	
PR	22-JUL-1999;	99US-0145089.	
PR	22-JUL-1999;	99US-0145192.	
PR	23-JUL-1999;	99US-0145145.	
PR	23-JUL-1999;	99US-0145218.	
PR	23-JUL-1999;	99US-0145224.	
PR	26-JUL-1999;	99US-0145276.	
PR	27-JUL-1999;	99US-0145913.	
PR	27-JUL-1999;	99US-0145918.	
PR	27-JUL-1999;	99US-0145919.	
PR	28-JUL-1999;	99US-0145951.	
PR	02-AUG-1999;	99US-0146386.	
PR	02-AUG-1999;	99US-0146388.	
PR	02-AUG-1999;	99US-0146389.	
PR	03-AUG-1999;	99US-0147038.	
PR	04-AUG-1999;	99US-0147204.	
PR	04-AUG-1999;	99US-0147302.	
PR	05-AUG-1999;	99US-0147192.	
PR	05-AUG-1999;	99US-0147260.	
PR	06-AUG-1999;	99US-0147303.	
PR	06-AUG-1999;	99US-0147416.	
PR	09-AUG-1999;	99US-0147935.	
PR	10-AUG-1999;	99US-0148171.	
PR	11-AUG-1999;	99US-0148319.	
PR	12-AUG-1999;	99US-0148341.	
PR	13-AUG-1999;	99US-0148565.	
PR	13-AUG-1999;	99US-0148684.	
PR	16-AUG-1999;	99US-0149368.	
PR	17-AUG-1999;	99US-0149175.	
PR	18-AUG-1999;	99US-0149426.	
PR	20-AUG-1999;	99US-0149722.	
PR	20-AUG-1999;	99US-0149723.	
PR	20-AUG-1999;	99US-0149929.	
PR	23-AUG-1999;	99US-0149902.	
PR	23-AUG-1999;	99US-0149930.	
PR	25-AUG-1999;	99US-0150566.	
PR	26-AUG-1999;	99US-0150884.	

PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.6%; Score 1030; DB 21; Length 339;
Best Local Similarity 63.3%; Pred. No. 1.3e-104;
Matches 214; Conservative 44; Mismatches 62; Indels 18; Gaps 7;
OY 1 MSVSCISDYDLICGEDSSGILGESP-ECFSFDIDSSPPPSPTTEDCYSIASFIERHN 59
Db 12 MSVSFSNDMDLFCGED-SGVFSGESTVDFFSSSEVDSWPGD-----SIACFIEDERH 61

[illegible]

RESULT 5	
AAG29790	
ID	AAG29790 standard; Protein; 320 AA.
XX	
AC	AAG29790;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35503.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	28-APR-1999; 99US-0130891.
PR	30-APR-1999; 99US-0131449.
PR	30-APR-1999; 99US-0132048.
PR	30-APR-1999; 99US-0132407.
PR	04-MAY-1999; 99US-0132484.
PR	05-MAY-1999; 99US-0132485.
PR	06-MAY-1999; 99US-0132486.
PR	06-MAY-1999; 99US-0132487.
PR	07-MAY-1999; 99US-0132863.
PR	11-MAY-1999; 99US-0134256.
PR	14-MAY-1999; 99US-0134218.
PR	14-MAY-1999; 99US-0134219.
PR	14-MAY-1999; 99US-0134221.
PR	14-MAY-1999; 99US-0134370.
PR	18-MAY-1999; 99US-0134768.
PR	19-MAY-1999; 99US-0134941.
PR	20-MAY-1999; 99US-0135124.

PR	21-MAY-1999;	99US-0135353
PR	24-MAY-1999;	99US-0135629
PR	25-MAY-1999;	99US-0136021
PR	27-MAY-1999;	99US-0136392
PR	28-MAY-1999;	99US-0136782
PR	01-JUN-1999;	99US-0137222
PR	03-JUN-1999;	99US-0137528
PR	04-JUN-1999;	99US-0137528
PR	07-JUN-1999;	99US-0137722
PR	08-JUN-1999;	99US-0138094
PR	10-JUN-1999;	99US-0138540
PR	14-JUN-1999;	99US-0138847
PR	16-JUN-1999;	99US-0139452
PR	16-JUN-1999;	99US-0139453
PR	17-JUN-1999;	99US-0139454
PR	18-JUN-1999;	99US-0139492
PR	18-JUN-1999;	99US-0139455
PR	18-JUN-1999;	99US-0139456
PR	18-JUN-1999;	99US-0139457
PR	18-JUN-1999;	99US-0139458
PR	18-JUN-1999;	99US-0139459
PR	18-JUN-1999;	99US-0139460
PR	18-JUN-1999;	99US-0139461
PR	18-JUN-1999;	99US-0139462
PR	18-JUN-1999;	99US-0139463
PR	18-JUN-1999;	99US-0139750
PR	18-JUN-1999;	99US-0139763
PR	21-JUN-1999;	99US-0139817
PR	22-JUN-1999;	99US-0140359
PR	23-JUN-1999;	99US-0140353
PR	23-JUN-1999;	99US-0140354
PR	24-JUN-1999;	99US-0140695
PR	28-JUN-1999;	99US-0140823
PR	29-JUN-1999;	99US-0140991
PR	30-JUN-1999;	99US-0141287
PR	01-JUL-1999;	99US-0141842
PR	01-JUL-1999;	99US-0142154
PR	02-JUL-1999;	99US-0142055
PR	06-JUL-1999;	99US-0142390
PR	08-JUL-1999;	99US-0142603
PR	09-JUL-1999;	99US-0142920
PR	12-JUL-1999;	99US-0142977
PR	13-JUL-1999;	99US-0143242
PR	14-JUL-1999;	99US-0143524
PR	15-JUL-1999;	99US-0144005
PR	16-JUL-1999;	99US-0144085
PR	16-JUL-1999;	99US-0144305
PR	19-JUL-1999;	99US-0144325
PR	19-JUL-1999;	99US-0144325
PR	19-JUL-1999;	99US-0144331
PR	19-JUL-1999;	99US-0144332
PR	19-JUL-1999;	99US-0144333
PR	19-JUL-1999;	99US-0144334
PR	19-JUL-1999;	99US-0144335
PR	20-JUL-1999;	99US-0144352
PR	20-JUL-1999;	99US-0144632
PR	20-JUL-1999;	99US-0144814
PR	21-JUL-1999;	99US-0144814
PR	21-JUL-1999;	99US-0145086
PR	21-JUL-1999;	99US-0145088
PR	22-JUL-1999;	99US-0145085
PR	22-JUL-1999;	99US-0145087
PR	22-JUL-1999;	99US-0145089
PR	22-JUL-1999;	99US-0145192
PR	23-JUL-1999;	99US-0145145
PR	23-JUL-1999;	99US-0145224
PR	23-JUL-1999;	99US-0145224
PR	26-JUL-1999;	99US-0145276
PR	27-JUL-1999;	99US-0145913
PR	27-JUL-1999;	99US-0145918
PR	27-JUL-1999;	99US-0145919
PR	28-JUL-1999;	99US-0145951
PR	02-AUG-1999;	99US-0146386

PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 57.5%; Score 1011; DB 21; Length 320;
Best Local Similarity 63.5%; Pred. No. 1.5e-102;
Matches 209; Conservative 43; Mismatches 59; Indels 18; Gaps 7;

QY 10 DLICGEDSSGILSGESP-ECSPSDIDSSPPPSPTTEDCYSIASFIEHERNFYGFEEYLS 68
DB 2 DLFCGED-SGVFSGESTVDFSSSEVDSPMGD-----SIACFIEDERHFPVGHLYLS 51
QY 69 RFQSRSLDANAREESVGVILKVHAYYGFQPLTAYLAVNMDRFLDSRRLPETNGMPLQLY 128
DB 52 RFQTRSLDASAREDSVAMILKVQAYYNEOPLTAYLAVNMDRFLYARRLPETSGMPMQLL 111
QY 129 SVACISLAKMEEPILVPSLIDQIEGAKYIFEPRTIRMEILLVGLDWRLRSVTPLCFL 108
DB 112 AVACISLAKMEEILVPSLFDPOVAGVKYLFPAKTIRKMEILLVSLDWRLRSVTPDEFI 171
QY 189 AEFACKYDSTGTGFIRFLISRATETIIVSNIOEASFILAYMPSCIAAAAILTAANEIPNW-SV 247
DB 172 SFPAYKIDPSGTFLGFFISHATEIILSNIKEASFLEWMPSSIAAAAILCVANELPSLSSV 231
QY 248 VKP-ENAESWCCEGLRKEKVICGYQLMOELVINNMOKPLPLKVLPLQRLVYTRTRMRSSTV 306
DB 232 VNPHESPETWCDGLSKEKIVRCYRLKMAIENNRLNTP--KVIAKLRSVRA---SSTL 286
QY 307 SSFSSSSSTSFSLSCRRKRLNRLWVDK 335
DB 287 TRPSDESSSFSSSPCKRRKLSGYSWGDE 315

RESULT 6
AA79321
ID AAY79321 standard; Protein; 358 AA.
AC AAY79321;
XX 18-JUL-2000 (first entry)
DT Maize cyclin D.
DE Maize cyclin D.
XX Maize; cyclin D; ZmCycd; Cycd; cell division; cell cycle;
KW transgenic plant.
XX Zea mays.
OS WO200017364-A2.
PN 30-MAR-2000.
PD 21-SEP-1999; 99WO-US21946.
PF 23-SEP-1998; 98US-0101551.
PR (PION-) PIONEER HI-BRED INT INC.
PA Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
PI Hoerster GJ;
XX WPI; 2000-283589/24.
DR N-PSDB; AA294581.
DR Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
PT related proteins and antisense RNA useful for control of cell cycle
PT regulation -
XX Claim 16; Page 117-118; 134pp; English.
PS The present sequence is that of an isoform of maize cyclin D
CC (Cycd), a protein necessary for progression from G1 into S phase.
CC

CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. All claimed.

SQ Sequence 358 AA;

Query Match	28.6%;	Score 502.5;	DB 21;	Length 358;
Best Local Similarity	34.0%;	Pred. No. 1.9e-46;		
Matches 131; Conservative	60;	Mismatches 99;	Indels 95;	Gaps 11;

QY 9 YD---LCCGDSGI-LGSESPCESFSDIDSSPPPT----- 43

Db 5 YDCAASVLLCAEDNAIILGLDDGEESWA--AAATPPRDTVAAAAATGVAVDGILTEF 61

0Y 44 --TEDCYSIASFIEHERNFVPGFEYLSRFQSRSD--ANAREESVGWILKVHAYYGFQ 97

Db 62 PLSDDC--VATLVEKEVEHMPAEGYLQKLQRHGDLDLAVRKDAIDWIKVIEHYNFA 11

98 PLIAYLVNMYDRFLDSRRLPETNGMPLQLSVACLSIAKMEEPVPSLLDQIEGAKY 15

DB 120 PLIAYLSVNI LDRFLS IYER PEGRAMMIQ LLA VACLS LASKI EETI FVPLPBDLQVAEAKF 17

02 100 IF E F R I N K M E L L V G V D M K R N S V I P L C F L A F A C K V D S I G T F I R F L I S K A I E I I V S N L 21

20 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1

DATE	TIME	LOCATION	ACTIVITY	REMARKS
12	1400	SEA	SEARCH	NO RESULTS
13	1400	SEA	SEARCH	NO RESULTS
14	1400	SEA	SEARCH	NO RESULTS
15	1400	SEA	SEARCH	NO RESULTS
16	1400	SEA	SEARCH	NO RESULTS
17	1400	SEA	SEARCH	NO RESULTS
18	1400	SEA	SEARCH	NO RESULTS
19	1400	SEA	SEARCH	NO RESULTS
20	1400	SEA	SEARCH	NO RESULTS
21	1400	SEA	SEARCH	NO RESULTS
22	1400	SEA	SEARCH	NO RESULTS
23	1400	SEA	SEARCH	NO RESULTS
24	1400	SEA	SEARCH	NO RESULTS
25	1400	SEA	SEARCH	NO RESULTS
26	1400	SEA	SEARCH	NO RESULTS
27	1400	SEA	SEARCH	NO RESULTS
28	1400	SEA	SEARCH	NO RESULTS
29	1400	SEA	SEARCH	NO RESULTS
30	1400	SEA	SEARCH	NO RESULTS
31	1400	SEA	SEARCH	NO RESULTS

[illegible]

— — — — —

RESULT 7
RAY70333

LD AAY/9322 standard; Protein; 358 AA.
XX

HA1/9322;
AC
XX

DT 18-JUL-2000 (first entry)

DE Maize cyclin D.

KW Maize; cyclin D; ZmCYCD; CYCD; cell division; cell cycle; transgenic plant.

05 Zea mays.

PN W0200017364-A2.

PD 30-MAR-2000.

PF 21-SEP-1999; 99WO-US21946.

PR 23-SEP-1998; 98US-0101551.

PA (PION-) PIONEER HI-BRED INT INC.
 VV

PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
PI Houston CT;

XX WPT: 2000-283589/2A
DB

DR N-PSDB; AAZ94582.
XX

PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
PT related proteins and antisense RNA useful for control of cell cycle
PT regulation -

PS Claim 16; Page 121-122; 134pp; English.

The present sequence is that of an isoform of maize cyclin D (Cycd), a protein necessary for progression from G1 into S phase. Cycd binds to CDK4, and the active Cycd-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize Cycd polynucleotides (see AA294581-84) and polypeptides (see AAY9321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycd in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of Cycd protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a Cycd polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the Cycd protein in the cell. The Cycd protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of Cycd protein in the cells is transiently modulated by introducing Cycd RNA or Cycd polypeptides. All claimed.

SQ **Sequence** **358 AA;**

Query Match	28.28;	Score 496.5;	DB 21;	Length 358;
Best Local Similarity	33.8%;	Pred. No. 8.8e-46;		
Matches 130; Conservative	60;	Mismatches 100;	Indels 95;	Gaps 11

```

QY 9 YD-----LTCGESSGT--LSGESPECSFDIDSSPPPSPT-----43
  |||:::|:|:::|

```

Db 5 YDCAASVLLCAEDNNAIIGLDDGEESSNA---AAATPRDTVAANAATGVAVDGILTEF 61
QY 44 ---TEDCYSIASFIEHERNFVPGFEYLSRQSRSLDAN---AREESVGMILKVHAYYGFQ 97
Db 62 PLLSDDC--VATLVEKEVEHMPAEGYLQKLRHGGDLLVAVRKDAIDWIKVIEHYNFA 119
QY 98 PLTAYLAVNYMDRFLDSRRLPETNGWPLQVSVACLSLAKMEEPVPSLIDLOIEGAKY 157
Db 120 PLTAVLSVNYLDRFLSTYEFEPEGRAWMTQLLAVACLSLASKIEETFEVPLFLDLQVAEAKF 179
QY 158 IFEPTIRRMELLVGLVDWRLRSVTPLCFLAFACKVDSTGTFFIRFLISRATEIIVSNI 217
Db 180 VFEGRTIKRMELLVSTLTKWRMHAVTACSEVEYFLHKLSDHGAPSLIARSSDLVLSTA 239
QY 218 QEASFLAYWPSCIAAAAILTANETPNMSVVKPENAESWCCEGLRKEKYGICQLOMQLVI 277
Db 240 KGAETVFRPSEIATAAVALAIGECRS-SVI--ERAASSCKYLDKERYLNCEMIQE--- 293
QY 278 NNNQRKLPLKVLPLQVLTTRTRTRMRSSSTVSSFS--- 311
Db 294 -----KITMGSIVLKSAAGSSISVSPQSPIGVLDAACISQSDATVGS 337
QY 312 -----SSSTSFSLCKRRKLNRL 330
Db 338 PAVCYHSSSTS-----KRRMITRRL 357

RESULT 8
AAY79323
ID AAY79323 standard; Protein; 390 AA.
XX AAY79323;
AC AAY79323;
DT 18-JUL-2000 (first entry)
XX
DE Maize cyclin D.
XX
KW Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
KW transgenic plant.
XX
OS Zea mays.
XX PN WQ200017364-A2.
XX
PD 30-MAR-2000.
XX
PF 21-SEP-1999; 99WO-US21946.
XX
PR 23-SEP-1998; 98US-0101551.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;
PI Hoerster GJ;
XX
DR WPI: 2000-283589/24.
DR N-PSDB; AA294583.
XX
PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
PT related proteins and antisense RNA useful for control of cell cycle
PT regulation -
XX
PS Claim 16; Page 124-125; 134pp; English.
XX
CC The present sequence is that of an isoform of maize cyclin D
CC (CycD), a protein necessary for progression from G1 into S phase.
CC CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates
CC retinoblastoma associated protein, releasing the E2F transcription
CC factor which activates DNA synthesis. The invention provides maize
CC CycD polynucleotides (see AA294581-84) and polypeptides (see
CC AA79321-24) that are involved in cell cycle regulation. Also provided
CC are recombinant expression cassettes (including ZmCycD in sense or
CC antisense orientation), host cells, transgenic plants (especially

CC corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or
CC oilseed Brassica) and antibody compositions. A claimed method of
CC modulating the level of CycD protein in a cell comprises.
CC transforming the cell with a recombinant expression cassette
CC comprising a CycD polynucleotide linked to a promoter, and
CC growing the cell for a time sufficient to induce expression of the
CC polynucleotide sufficient to modulate (increase or decrease) the
CC CycD protein in the cell. The CycD protein is present in an amount
CC sufficient to alter cell division, increase the number of cells
CC dividing, improve transformation frequencies, alter cell growth,
CC increase the growth rate, increase crop yield, alter plant
CC height or size, enhance or inhibit organ (seed, root, shoot, ear,
CC tassel, stalk, pollen, stamen) growth, produce organ ablation,
CC produce parthenocarpic fruits, produce male sterile plants,
CC enhance embryogenic response, increase callus induction, provide
CC positive selection, increase plant regeneration, alter the time
CC that cells are arrested in G1 or G0 phase or in a particular cell
CC cycle, improve response to environmental stress including
CC dehydration, heat or cold, increase the number of pods per plant,
CC increase the number of seeds per pod or ear, alter the lag time in
CC seed development, provide hormone-independent cell growth, or
CC increase the growth rate of cells in bioreactors. The level of
CC CycD protein in the cells is transiently modulated by introducing
CC CycD RNA or CycD polypeptides. All claimed.

Sequence 390 AA;

Query Match 26.7%; Score 470; DB 21; Length 390;
Best Local Similarity 33.6%; Pred. No. 8.3e-43;
Matches 130; Conservative 59; Mismatches 124; Indels 74; Gaps 13;

QY 1 MSVSCISDYD-----LLCGEDSSGIL-----SGESPECSFSD---IDSSP 37
Db 1 MAPSC---YDAASMLLCAEEHSSILMYDEEBEELAVGRRGRSP--GYGDDFGADLEP 55
QY 38 PPPSPTEDECYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESVGMILKVHAYYGFQ 97
Db 56 ----POSEEC--VAGLVERERDHPMPCCYCDRLRGCGGCLCYRREAVDWIKAYTHRRFR 109
QY 98 PLTAYLAVNYMDRFLDSRRLPETNGWPLQVSVACLSLAKMEEPVPSLIDLOIEGAKY 157
Db 110 PLTAYLAVNYLDRFLSLSEVPDCKDMTQLLAVACVSLAKMEETAVPQCLDLOVGDAKY 169
QY 158 IFEPTIRRMELLVGLVDWRLRSVTPLCFLAFACKVDSTGTFT--RFLISRATEIIVS 215
Db 170 VFEAKTVQRMELLVLTTLNWRMHAVTPESSVDYFLNKLISNGGTAAPRSCWLLQSAELLIR 229
QY 216 NIQASFLAYWPSCIAAAAILTANETPNMSVVKPENAESWCCEGLRKEKYGICQLOMQL 275
Db 230 AARGTGVCFRPSSEIATAAVALAAGVDVDADGV--ENA--CCAHYDKERVLRCQEAIGSM 285
QY 276 V-----INNQRKLPLKVLPLQVLTTRTRMR 302
Db 286 ASSAIDGATVPPKSARRRSSPVVPVQSPVGLDAACLSYRSEEAATATATSA 345
QY 303 SSTVSSFSSSSTSFSLSCKRRKLNMR 329
Db 346 SHGPPGSSSSSTS--PVTSKRRKLASR 371

RESULT 9
AAY31897
ID AAY31897 standard; Protein; 388 AA.
XX
AC AAY31897;
XX
DT 21-DEC-1999 (first entry)
XX
DE Corn cyclin delta-2 partial polypeptide.
XX
KW Cyclin delta-2; corn; maize; cell cycle; cell division;
KW transgenic plant; herbicide; plant breeding.
XX

QY 308 --SFSSSSSTFSLCKRRLNR 329
|||||.. .. |||||.

Db 346 GAPSSSSSTSPVTSKRRLASR 369

**C
1
E
T
T
E
C**

AA647103 standard: protein: 308 AA

XX 23047103.

XX
XX
XX

10 000 000 + 000 000

XX 4414000 fragment SEQ ID NO. 593333

transduction pathway: metabolic pathway:

Protein identification; signal transduction pathway; metabolic pathway; hybridization assay; genomic mapping; gene expression control; promoter

termination sequence.
KW
XX

XX
XX
XX

XX	06-SEP-2000.
PD	
XX	
PF	25-FEB-2000; 2000EP-0301439.

PR	30-APR-1999;	99US-0132407
PR	04 MAY 1999;	00US-0132484

PR	05-MAY-1999;	99US-0132485
PR	06-MAY-1999;	99US-0132486
PR	06-MAY-1999;	99US-0132487
PR	07-MAY-1999;	99US-0132488

PR 11-MAY-1999; 99US-0134256
PR 14-MAY-1999; 99US-0134218
PR 14-MAY-1999; 99US-0134219
PR 14-MAY-1999; 99US-0134221

PR 14-MAY-1999; 99US-0134370
PR 18-MAY-1999; 99US-0134768
PR 19-MAY-1999; 99US-0134941

PR	21-MAY-1999;	99US-0135353
PR	24-MAY-1999;	99US-0135629

PR 28-MAY-1999; 99US-0136782

PR	04-JUN-1999;	99US-0137502
----	--------------	--------------

PR 10-JUN-1999; 99US-0138540
10 JUN 1999; 00US-0138947

PR	16-JUN-1999;	99US-0139452
PR	16-JUN-1999;	99US-0139453

PR 16-JUN-1999; 99US-01394923
PR 17-JUN-1999; 99US-01394922

PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139457.
PR	18-JUN-1999;	99US-0139458.
PR	18-JUN-1999;	99US-0139459.
PR	18-JUN-1999;	99US-0139460.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	22-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	19-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	03-AUG-1999;	99US-0147038.
PR	04-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	05-AUG-1999;	99US-0147392.
PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.

PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-01494175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149930.
PR	23-AUG-1999;	99US-0149932.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	30-AUG-1999;	99US-0151080.
PR	31-AUG-1999;	99US-0151303.
PR	01-SEP-1999;	99US-0151438.
PR	07-SEP-1999;	99US-0151930.
PR	10-SEP-1999;	99US-0152363.
PR	13-SEP-1999;	99US-0153070.
PR	15-SEP-1999;	99US-0153758.
PR	16-SEP-1999;	99US-0154018.
PR	20-SEP-1999;	99US-0154039.
PR	22-SEP-1999;	99US-0154779.
PR	23-SEP-1999;	99US-0155139.
PR	24-SEP-1999;	99US-0155486.
PR	28-SEP-1999;	99US-0155659.
PR	29-SEP-1999;	99US-0156458.
PR	04-OCT-1999;	99US-0156596.
PR	05-OCT-1999;	99US-0157117.
PR	06-OCT-1999;	99US-0157753.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161922.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

[illegible]

PR	06-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	09-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	10-AUG-1999;	99US-0148171.
PR	11-AUG-1999;	99US-0148319.
PR	12-AUG-1999;	99US-0148341.
PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

	Matches	107;	Conservative	57;	Mismatches	101;	Indels	35;	Gaps	7;									
OY	55	EHERNFVPGFEYL	SFRQSRSLDANARESVGWLKVHAYYGQPLTAYLAVNYMDRELDS	114	:	:	:	:	:	:									
Db	16	ENETNPCFGEQILDGFL	-----VSCRKALDWLVLRVKSHYGFTSLTAILAVNYFDRENTS	70	:	:	:	:	:	:									
OY	115	RRLPETNGWPLQLVSVACLSLAAKMEELPVSLDLQIEGAKYIFEPRTIRRMELLVLGV	174	:	:	:	:	:	:	:									
Db	71	IKLGTDKPWMSQJLVAVASLSLAKEVEIQVPLLLDLOVEEARLYFEAKTIQRMELLIST	130	:	:	:	:	:	:	:									
OY	175	LDMRLRSVTPLCF	----LAFACKVDSTGTGFIRFLISRATETIVSNIOEASFAYWPSCI	230	:	:	:	:	:	:									
Db	131	LQWRMHPVTPISPFDDHIIRREGSKWHQQLDFCR	---KCERLLISVIADTRFMRYPPSVL	186	:	:	:	:	:	:									
OY	231	AAAAILTAANEIPNWSVVKPENAESWCEDLRKEKVGICYOQLMOELVINNOQRKLPLIKVL	290	:	:	:	:	:	:	:									
Db	187	ATAIMILVFEEELRCDEVEYQSQTITTLKVNQEKVNECY	---ELLEHNPSKKRMMNLV	242	:	:	:	:	:	:									
OY	291	PQ-----LRVTTTRTRMRSSTVSSFSSSSSSTSFSLSCRRKLN	-----NRLEWD	333	:	:	:	:	:	:									
Db	243	QQDSPSGVLDFDDSSNSSSWNVSTTASYSSSSSSPEPL-LKRRRVQEQOMRLPSINRMFLD	301	:	:	:	:	:	:	:									
RESULT 12																			
ID	AAG23946	standard; Protein; 367 AA.																	
XX	AC	AAG23946;																	
XX	DT	17-OCT-2000 (first entry)																	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 27438.																		
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.																		
OS	Arabidopsis thaliana.																		
PN	EP1033405-A2.																		
PD	06-SEP-2000.																		
PF	25-FEB-2000; 2000EP-0301439.																		
PR	25-FEB-1999;	99US-0121825.																	
PR	05-MAR-1999;	99US-0123180.																	
PR	09-MAR-1999;	99US-0123548.																	
PR	23-MAR-1999;	99US-0125788.																	
PR	25-MAR-1999;	99US-0126264.																	
PR	29-MAR-1999;	99US-0126785.																	
PR	01-APR-1999;	99US-0127462.																	
PR	08-APR-1999;	99US-0128234.																	
PR	16-APR-1999;	99US-0129845.																	
PR	19-APR-1999;	99US-0130077.																	
PR	21-APR-1999;	99US-0130449.																	
PR	23-APR-1999;	99US-0130510.																	
PR	28-APR-1999;	99US-0131449.																	
PR	30-APR-1999;	99US-0132048.																	
PR	04-MAY-1999;	99US-0132484.																	
PR	05-MAY-1999;	99US-0132485.																	
PR	06-MAY-1999;	99US-0132486.																	

PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.

PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match	23.98;	Score 419.5;	DB 21;	Length 367;
Best Local Similarity	35.78;	Pred. No. 2.8e-37;		
Matches 107; Conservative	57;	Mismatches 101;	Indels 35;	Gaps 7;

QY	55	EHERNEFVPEFEYLSRFQSRSLDANAREESVGWILKVHAYYGFOPLTAYLAVNMDRFLDS	114
Db	76	ENETNPCEGEQILDGFL-----VSCRKALDWLVKRVKSHYGTSLTALAVNYFDREMTS	130
QY	115	RRLPETNGMPLQOLVSVACLSLAAKMEPPLVPSLLDQIEBAAKYYIEFPRTIRRMELLVLGV	174
Db	131	IKLODKPMNSQOLVAVASLSLAAKVEEIQVPLLLDLQVEBARYLFEAKTIQRMELLILST	190
QY	175	LDMRLRSVTPLCF---LAEFACKVDSTGTGFIRELLISRATEIIVSNIOEASFAYWPSCI	230
Db	191	LQWRMHPVTPISFEDHIIRRFGSKWHQQLDFCR---KCERLISVIADTRFMRYFPSVL	246
QY	231	AAAAILFANEIIPNWSVVKPENAESWCEGLRKEKVGICQOLMQLVINNNQORKPLLVKL	290
Db	247	ATAIMILVFEEELKPCDEVEYEQSQITLLKVNQEKVNECY----ELLLEHNPSKRRMNULV	302
QY	291	PQ-----LRYTTRTRMRSSIVSESSSSSSTFSLSCKRRKLN-----NRLLWVD	333
Db	303	DQDSPSGVLDFFDDSSNSSNWNVSTTASVSSSSSSPEPL-LKRRRVQEQOMRLPSINDMFLD	361

RESULT 13
AAG23337
ID AAG23337 standard; Protein; 308 AA.

AC	AAG23337;	
XX		
DT	17-OCT-2000	(first entry)
XX		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 26608.	
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.	
KW		

PR	06-MAY-1999;	99US-0132486;
PR	06-MAY-1999;	99US-0132487;
PR	07-MAY-1999;	99US-0132863;
PR	11-MAY-1999;	99US-0134256;
PR	14-MAY-1999;	99US-0134218;
PR	14-MAY-1999;	99US-0134219;
PR	14-MAY-1999;	99US-0134321;
PR	18-MAY-1999;	99US-0134370;
PR	19-MAY-1999;	99US-0134941;
PR	20-MAY-1999;	99US-0135124;
PR	21-MAY-1999;	99US-0135353;
PR	24-MAY-1999;	99US-0135629;
PR	25-MAY-1999;	99US-0136021;
PR	27-MAY-1999;	99US-0136392;
PR	28-MAY-1999;	99US-0136782;
PR	01-JUN-1999;	99US-0137222;
PR	03-JUN-1999;	99US-0137528;
PR	04-JUN-1999;	99US-0137502;
PR	07-JUN-1999;	99US-0138074;
PR	08-JUN-1999;	99US-0138540;
PR	10-JUN-1999;	99US-0138540;
PR	10-JUN-1999;	99US-0138847;
PR	14-JUN-1999;	99US-0139119;
PR	16-JUN-1999;	99US-0139453;
PR	16-JUN-1999;	99US-0139453;
PR	17-JUN-1999;	99US-0139452;
PR	18-JUN-1999;	99US-0139454;
PR	18-JUN-1999;	99US-0139455;
PR	18-JUN-1999;	99US-0139456;
PR	18-JUN-1999;	99US-0139457;
PR	18-JUN-1999;	99US-0139458;
PR	18-JUN-1999;	99US-0139459;
PR	18-JUN-1999;	99US-0139460;
PR	18-JUN-1999;	99US-0139461;
PR	18-JUN-1999;	99US-0139462;
PR	18-JUN-1999;	99US-0139463;
PR	18-JUN-1999;	99US-0139750;
PR	18-JUN-1999;	99US-0139763;
PR	21-JUN-1999;	99US-0139817;
PR	22-JUN-1999;	99US-0139899;
PR	23-JUN-1999;	99US-0140353;
PR	23-JUN-1999;	99US-0140354;
PR	24-JUN-1999;	99US-0140695;
PR	28-JUN-1999;	99US-0140823;
PR	29-JUN-1999;	99US-0140991;
PR	30-JUN-1999;	99US-0141287;
PR	01-JUL-1999;	99US-0141842;
PR	01-JUL-1999;	99US-0142154;
PR	02-JUL-1999;	99US-0142055;
PR	06-JUL-1999;	99US-0142390;
PR	08-JUL-1999;	99US-0142803;
PR	09-JUL-1999;	99US-0142920;
PR	12-JUL-1999;	99US-0142977;
PR	13-JUL-1999;	99US-0143542;
PR	14-JUL-1999;	99US-0143624;
PR	15-JUL-1999;	99US-0144005;
PR	16-JUL-1999;	99US-0144085;
PR	16-JUL-1999;	99US-0144086;
PR	19-JUL-1999;	99US-0144325;
PR	19-JUL-1999;	99US-0144331;
PR	19-JUL-1999;	99US-0144332;
PR	19-JUL-1999;	99US-0144333;
PR	19-JUL-1999;	99US-0144334;
PR	19-JUL-1999;	99US-0144335;
PR	20-JUL-1999;	99US-0144352;
PR	20-JUL-1999;	99US-0144632;
PR	20-JUL-1999;	99US-0144684;
PR	21-JUL-1999;	99US-0144814;
PR	21-JUL-1999;	99US-0145086;
PR	21-JUL-1999;	99US-0145088;
PR	22-JUL-1999;	99US-0145085;
PR	22-JUL-1999;	99US-0145087;

PR	22-JUL-1999;	99US-0145089;
PR	22-JUL-1999;	99US-0145192;
PR	23-JUL-1999;	99US-0145145;
PR	23-JUL-1999;	99US-0145218;
PR	23-JUL-1999;	99US-0145224;
PR	26-JUL-1999;	99US-0145276;
PR	27-JUL-1999;	99US-0145913;
PR	27-JUL-1999;	99US-0145918;
PR	27-JUL-1999;	99US-0145919;
PR	28-JUL-1999;	99US-0145951;
PR	02-AUG-1999;	99US-0146386;
PR	02-AUG-1999;	99US-0146388;
PR	02-AUG-1999;	99US-0146389;
PR	03-AUG-1999;	99US-0147038;
PR	04-AUG-1999;	99US-0147204;
PR	04-AUG-1999;	99US-0147302;
PR	05-AUG-1999;	99US-0147192;
PR	05-AUG-1999;	99US-0147260;
PR	06-AUG-1999;	99US-0147303;
PR	06-AUG-1999;	99US-0147416;
PR	09-AUG-1999;	99US-0147493;
PR	09-AUG-1999;	99US-0147935;
PR	10-AUG-1999;	99US-0148171;
PR	11-AUG-1999;	99US-0148319;
PR	12-AUG-1999;	99US-0148341;
PR	13-AUG-1999;	99US-0148565;
PR	13-AUG-1999;	99US-0148684;
PR	16-AUG-1999;	99US-0149368;
PR	17-AUG-1999;	99US-0149175;
PR	18-AUG-1999;	99US-0149426;
PR	20-AUG-1999;	99US-0149722;
PR	20-AUG-1999;	99US-0149723;
PR	20-AUG-1999;	99US-0149929;
PR	23-AUG-1999;	99US-0149902;
PR	23-AUG-1999;	99US-0149930;
PR	25-AUG-1999;	99US-0150566;
PR	26-AUG-1999;	99US-0150884;
PR	27-AUG-1999;	99US-0151065;
PR	27-AUG-1999;	99US-0151066;
PR	27-AUG-1999;	99US-0151080;
PR	30-AUG-1999;	99US-0151438;
PR	31-AUG-1999;	99US-0151438;
PR	01-SEP-1999;	99US-0151930;
PR	07-SEP-1999;	99US-0152363;
PR	10-SEP-1999;	99US-0153070;
PR	13-SEP-1999;	99US-0153758;
PR	15-SEP-1999;	99US-0154018;
PR	16-SEP-1999;	99US-0154039;
PR	20-SEP-1999;	99US-0154779;
PR	22-SEP-1999;	99US-0155139;
PR	23-SEP-1999;	99US-0155486;
PR	24-SEP-1999;	99US-0155659;
PR	28-SEP-1999;	99US-0156458;
PR	29-SEP-1999;	99US-0156596;
PR	04-OCT-1999;	99US-0157117;
PR	05-OCT-1999;	99US-0157753;
PR	06-OCT-1999;	99US-0157865;
PR	07-OCT-1999;	99US-0158029;
PR	08-OCT-1999;	99US-0158232;
PR	12-OCT-1999;	99US-0158369;
PR	13-OCT-1999;	99US-0159293;
PR	13-OCT-1999;	99US-0159294;
PR	13-OCT-1999;	99US-0159295;
PR	14-OCT-1999;	99US-0159329;
PR	14-OCT-1999;	99US-0159330;
PR	14-OCT-1999;	99US-0159331;
PR	14-OCT-1999;	99US-0159637;
PR	14-OCT-1999;	99US-0159638;
PR	18-OCT-1999;	99US-0159584;
PR	21-OCT-1999;	99US-0160741;
PR	21-OCT-1999;	99US-0160767;
PR	21-OCT-1999;	99US-0160768;
PR	21-OCT-1999;	99US-0160770;

PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

```

Query Match          23.8%; Score 418.5; DB 21; Length 308;
Best Local Similarity 35.5%; Pred. No. 2.8e-37;
Matches 97; Conservative 51; Mismatches 84; Indels 41; Gaps 7;

QY      8 DYDLICE---DSSGILSGES-----PCSFSDDIDSSPPPSPTTEDCYSIASFIEHER 58
          : ||| | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      7 ELSLCTESNVDDGEMIVDETPIETISIPQMGFSQSESE-----IIMEMVEKER 55

QY      59 NEVPGHEVYLSRFQSRSLDAN-AREBSVGWILKVHAYYGFOPLTAYIAVNYMDRELDSRRL 117
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      56 QHLPSSDYIKRLRSGDDLNVGRDALNMIWKACEVHQFGPFCCLAMNYLDRLSVHDL 115

QY      118 PETNGWPLQLVSVACLSLAAKMEELVPSLLDQIEGAKYIFEBRTIRRMELLVLGLDW 177
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd      116 PSKGKWLQLLAVACLSLAKIEETVPMILIDLQVGDPQVFVEAKSVQRMELLVLNRLKW 175

QY      178 RLRSVTPPLCFLAF-----ACKVDSNGTFIRFLISRATEIIVSNIOEASFLAYWPSCIAA 232
          ||| : || : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      176 RLRAITPCSYIRYFLRKMSKCDQEPSNT----LISRSLOVIASITTKGIDFLEFRPSEVAA 231

QY      233 AAILTANET-----PNMSVVKPENAE 254
          | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd      232 AVALSVSGELQRVHFDNSSFSPLESLLOKERVK 264

```

RESULT 14	
ACG07075	
ID	AAG07075 standard; Protein; 361 AA.
XX	
AC	AAG07075;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 4088.
XX	
KW	protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.

PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.

PR	14-OCT-1999;	99US-01593330.
PR	14-OCT-1999;	99US-01593331.
PR	14-OCT-1999;	99US-01596337.
PR	14-OCT-1999;	99US-01596338.
PR	18-OCT-1999;	99US-01595884.
PR	21-OCT-1999;	99US-01607411.
PR	21-OCT-1999;	99US-01607657.
PR	21-OCT-1999;	99US-01607668.
PR	21-OCT-1999;	99US-01607770.
PR	21-OCT-1999;	99US-01608114.
PR	21-OCT-1999;	99US-01608015.
PR	22-OCT-1999;	99US-01609801.
PR	22-OCT-1999;	99US-01609881.
PR	22-OCT-1999;	99US-01609889.
PR	25-OCT-1999;	99US-01614004.
PR	25-OCT-1999;	99US-01614005.
PR	25-OCT-1999;	99US-01614006.
PR	26-OCT-1999;	99US-01613359.
PR	26-OCT-1999;	99US-01613601.
PR	26-OCT-1999;	99US-01613661.
PR	28-OCT-1999;	99US-01619920.
PR	28-OCT-1999;	99US-01619931.
PR	29-OCT-1999;	99US-01621422.

Query Match	23.4%;	Score 411;	DB 21;	Length 361;
Best Local Similarity	31.4%;	Pred. No. 2.4e-36;		
Matches 109;	Conservative 59;	Mismatches 119;	Indels 60;	Gaps 7;

[illegible]

RESULT 15	
AAG53864	
ID	AAG53864 standard; Protein; 361 AA.
XX	
AC	AAG53864;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 68617.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter::
XX	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.

XX	25-FEB-2000;	2000EP-0301439.
XX	25-FEB-1999;	99US-0121825.
PR	05-MAR-1999;	99US-0122180.
PR	09-MAR-1999;	99US-0122548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	06-APR-1999;	99US-0128234.
PR	16-APR-1999;	99US-0128714.
PR	19-APR-1999;	99US-0129845.
PR	21-APR-1999;	99US-0130077.
PR	23-APR-1999;	99US-0130449.
PR	28-APR-1999;	99US-0130510.
PR	28-APR-1999;	99US-01310891.
PR	30-APR-1999;	99US-0131449.
PR	30-APR-1999;	99US-0132048.
PR	30-APR-1999;	99US-0132407.
PR	04-MAY-1999;	99US-0132484.
PR	05-MAY-1999;	99US-0132486.
PR	06-MAY-1999;	99US-0132485.
PR	06-MAY-1999;	99US-0132487.
PR	07-MAY-1999;	99US-0132863.
PR	11-MAY-1999;	99US-0134256.
PR	14-MAY-1999;	99US-0134218.
PR	14-MAY-1999;	99US-0134219.
PR	14-MAY-1999;	99US-0134221.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135629.
PR	25-MAY-1999;	99US-0136021.
PR	27-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
PR	03-JUN-1999;	99US-0137528.
PR	04-JUN-1999;	99US-0137524.
PR	07-JUN-1999;	99US-0137724.
PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
PR	10-JUN-1999;	99US-0138847.
PR	14-JUN-1999;	99US-0139119.
PR	16-JUN-1999;	99US-0139452.
PR	16-JUN-1999;	99US-0139453.
PR	17-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
PR	18-JUN-1999;	99US-0139456.
PR	18-JUN-1999;	99US-0139461.
PR	18-JUN-1999;	99US-0139462.
PR	18-JUN-1999;	99US-0139463.
PR	18-JUN-1999;	99US-0139750.
PR	18-JUN-1999;	99US-0139763.
PR	21-JUN-1999;	99US-0139817.
PR	22-JUN-1999;	99US-0139899.
PR	23-JUN-1999;	99US-0140353.
PR	23-JUN-1999;	99US-0140354.
PR	24-JUN-1999;	99US-0140695.
PR	28-JUN-1999;	99US-0140823.
PR	29-JUN-1999;	99US-0140991.
PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.

PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.

PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 23.4%; Score 411; DB 21; Length 361;
Best Local Similarity 31.4%; Pred. No. 2.4e-36;
Matches 109; Conservative 59; Mismatches 119; Indels 60; Gaps 7;

QY 6 LSDYDLGEGDSGLISGESPECSFSDDIDSSPPPTTEDCYSIASFIEHERNFVPGFE 65
Db 49 LSDHDMWDDDELSTLISKQEPCLYDEI-----LDD-----E 80
QY 66 YLSRFQSRSLDANARESVGWLKVHAYVGFOPLTAYLAVNYMDRFLDSRRLPETNGWPL 125
Db 81 FL-----VLCREKALDWIFKVKSHYGFNSLTALLAVNYFDRFTSRKFGQTDKPMWS 131
QY 126 QLVSVACLSLAAKMEEPVPSLLDLQIEGAKYIFEPRTIRMEELVLYGLDWRILRSVPL 185
Db 132 QLTALACLSIAAKVEETIRVPFLDFOVEEARVYEAKTIQRMELVLSLTDWRMHVPPI 191
QY 186 CFLAFACKVDSTGTIFIRFLISRATEIIVSNTQEASFAYWPSCIAAAILTAANEIPNW 245
Db 192 SFDHIIRRYSEFKSHQLEFLSRCESLLSTIPDSRFLSFSPSVLATATMWSVIRDLKMC 251
QY 246 SVVKPENAESWCEGLREKVIQCYQLMOELVINNQKRLPLKVLPPQ----LRVTTTRTM 301
Db 252 DEAVYQSQIMTLTKVDSEKVNKCY---ELVLDHSPSKKRMNMNMQOPASPIGVFDASFS 307
QY 302 RSSTVSSFSSSSSTSPSLS-----CKRRKLN-----NRLWVD 333
Db 308 SDDSNSWVVSASASVSSPSPSEPLKRRRVQEQQRLSSINRMFFD 354

Search completed: October 23, 2002, 14:38:10
Job time : 36 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:36:49 : Search time 18 Seconds
(without alignments)
1809.682 Million cell updates/sec

Title: US-09-665-308D-12

Perfect score: 1758

Sequence: 1 MSVSCSLDYDLLCGEDSSGI.....SCKRRKLNRLMWDDKGNSE 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1030	58.6	339	2	A96725	hypothetical prote
2	949.5	54.0	334	2	S51650	cyclin delta-1 - A
3	463.5	26.4	372	2	T09961	cyclin D-like prot
4	451	25.7	361	2	C84613	probable cyclin D
5	444	25.3	383	2	S51651	cyclin delta-2 - A
6	416	23.7	376	2	T05420	cyclin delta-3 - A
7	411	23.4	361	2	T45860	cyclin D3-like pro
8	368	20.9	317	2	T49995	cyclin protein-lik
9	367	20.9	386	2	T09598	cyclin 4, D-type -
10	340.5	19.4	302	2	E85041	probable D-type cy
11	276	15.7	321	2	T04720	hypothetical prote
12	247	14.1	454	2	A96803	probable mitotic c
13	244	13.9	341	2	T48232	hypothetical prote
14	228	13.0	502	2	T02746	cyclin A-like prot
15	220	12.5	456	2	C57742	cyclin II - maize
16	218.5	12.4	482	2	T02967	cyclin A-type (clo
17	216.5	12.3	483	2	T02966	cyclin A-type (clo
18	216.5	12.3	483	2	T03606	cyclin, A-type - c
19	208	11.8	446	2	T09960	mitosis-specific c
20	205.5	11.7	441	2	S41710	mitosis-specific c
21	205	11.7	443	2	T14916	mitosis-specific c
22	201	11.4	425	2	S53004	mitosis-specific c
23	200.5	11.4	452	2	T10527	cyclin B1d-11 - ye
24	200	11.4	328	2	S29925	cyclin 2 - alfalfa
25	200	11.4	434	2	T09706	cyclin cycms2, B-t
26	200	11.4	469	2	T07672	cyclin a2-type, ml
27	199	11.3	428	2	T04743	cyclin cycl - Arab
28	199	11.3	473	2	T03611	cyclin, B-type - c
29	198.5	11.3	491	2	S14166	cyclin B2 - yeast

30	197.5	11.2	454	2	S16522	mitosis-specific c
31	197	11.2	449	2	S49904	cyclin - common to
32	197	11.2	460	2	B86339	protein F2D10.10 l
33	196.5	11.2	341	2	S16521	mitosis-specific c
34	196.5	11.2	419	2	T03675	cyclin 2 - rice
35	196.5	11.2	471	2	S14165	cyclin B1 - yeast
36	196	11.1	398	2	T12530	hypothetical prote
37	195.5	11.1	493	2	T03609	cyclin, A-type - c
38	194.5	11.1	473	2	S41709	mitosis-specific c
39	193.5	11.0	446	2	T03021	mitosis-specific c
40	192	10.9	484	2	T07675	cyclin a2-type, ml
41	191.5	10.9	415	2	S1637	cyclin A2 - Africa
42	191	10.9	460	2	D96505	probable mitotic c
43	190	10.8	398	2	S21529	cyclin B2 - mouse
44	190	10.8	399	2	S23596	cyclin B2 - chicke
45	189.5	10.8	408	2	S17793	cyclin B - common

ALIGNMENTS

RESULT 1

A96725

hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96725

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: A96725

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-339 <STO>

A:Cross-references: GB:AE005173; NID:g2194121; PIDN:AAB61096.1; GSPDB:GN00141

C:Genetics:

A:Gene: F20P5.7

A:Map position: 1

Query Match

Best Local Similarity 58.6% Score 1030; DB 2; Length 339;

Matches 214; Conservative 44; Mismatches 62; Indels 18; Gaps 7;

Qy	1	MSVSCSLDYDLLCGEDSGILGESP-ECFSFSDIDSPPPSPPTTEDCYASIEHERN 59	: : :
Db	12	MSVSFNDMDLFCGED-SGVFSGESTVDFFSSSEVDSPG-----SIACFIEDERH 61	: : :
Qy	60	FVPGFEYLSRFOSRLDANAREESVGMILKVHAYYGFQPLTAYLAVNYMDRLDSRLPE 119	: : : : : : :
Db	62	FVPGHDYLSRFQTRSLDASAREDSVAMILKVQAYVNPQPLTAYLAVNYMDRLYARLPE 121	: : : : : : :
Qy	120	TNGWPIQLVSVACLSIAAKMEELVPSLLDQIEGAKYIEFRTIRRMELVGLDWRL 179	: : : : : : :
Db	122	TSGWPMQLLAVACLSIAAKMEELVPSLDFQVAGVYLLFEAKTIKRMELVSVLDWRL 181	: : : : : : :
Qy	180	RSVTPICFLAFACKVDSTGTFIRFLISRATEIIVSNIQEASFSLAYWPSCTAAAILTAA 239	: : : : : : :
Db	182	RSVTPIDFISFAFKIDPSGTFGLGFISHATEILSNIKENASFLYWPSSIAAAILCYA 241	: : : : : : :
Qy	240	NEIPNW-SVVKP-ENAESWCEGLRKEKVIQYQMLQELVINNNQKPLPLKVLPLQVTVT 297	: : : : : : :
Db	242	NELPSLSSVYNPHESPETWCDSKEKIVRCYRIKAMAIENNRLNTP--KVIAKLRVSV 299	: : : : : : :
Qy	298	RTMRSSTVSSSSSSSTSFSLCKRRKLNRLMWVDR 335	: : : : : : :

Db 300 RA---SSTLRPSDESSSSSPCKRRKLSGYSWGDE 334

RESULT 2

S51650

cyclin delta-1 - Arabidopsis thaliana

N:Alternate names: cyclin D homolog

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997

C:Accession: S51650

R:Soult, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.

submitted to the EMBL Data Library, December 1994

A:Description: A family of cyclin D homologs from plants differentially controlled by gr

A:Reference number: S51650

A:Accession: S51650

A:Molecule type: mRNA

A:Residues: 1-334 <SON>

A:Cross-references: EMBL:X83369; NID:g603504; PID:g603505

C:Keywords: cell cycle control; cell division control

Query Match

Best Local Similarity 54.0%; Score 949.5; DB 2; Length 334;

Matches 204; Conservative 44; Mismatches 67; Indels 23; Gaps 9;

QY 1 MSVSCLSYDYLIGEDSSGILSGESP-ECSESDIDSSPPPTEDCYSIASFIEHERN 59

Db 12 MSVSFSNDMDLFCGED-SGVFSGESTVDFSSSEVDSPGD-----SIACFIEDERT 61

QY 60 FVPGFEYLSRFSRLDANAREESVGTWKVHAYYGFOPLTAYLVNMDRFLDSRLPE 119

Db 62 FVPGHDYLSRFGTRSLDASAREDSVAVLKQAYYNFQPLSAVLAIVNMDRFLYARRLPE 121

QY 120 TNGWPLQLVAVACLSLAKMEPLVPSLIDQIEGAKYIFEPRTIRRMELLYLVGLDWR 179

Db 122 TSGWPMQLAVACLSLAKMEELVPSLEDFQVAGVKYLFKAKTIKRMELLYLVGLDWR 181

QY 180 RSVTPPLCLAFACKVDSTGTFFIRFLISRAEIIIVSNIGASFLAYWPSICIAAAITLTA 239

Db 182 RSVTPFDFISFAIKIDLRVPFSGSL-SPMLQISLNIKEASFLEYWPSISIAAAITLTA 240

QY 240 NEIPNW-SVVKP-ENAESWCGLRKEKYGICQYLMQELVINNNQKLPPLKVLPLQRLVT 297

Db 241 NELPSLSVAVNPHESPETWCDGLSKEKIVRCYRLKMAIENNRNLTNP--KVIKLRVSV 298

QY 298 RTRMRSSVSSSSSSSTSSLSCKRRKLNRLWVDDK 335

Db 299 RA---SSTLRPSDESSS---PCKRRKLSGYSWGDE 329

RESULT 3

T09961

cyclin D-like protein - red goosefoot

C:Species: Chenopodium rubrum (red goosefoot)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: T09961

R:Renzi, A.; Fountain, M.; Beck, E.

submitted to the EMBL Data Library, December 1996

A:Description: Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotr

A:Reference number: Z16906

A:Accession: T09961

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-372 <REN>

A:Cross-references: EMBL:X10162; NID:e1014005; PID:e290219

A:Experimental source: 7 day old culture; photoautotrophic cells derived from hypocotyl

C:Genetics:

A:Gene: cycD1

C:Keywords: cell cycle control; cell division control

Query Match

Best Local Similarity 26.4%; Score 463.5; DB 2; Length 372;

Matches 120; Conservative 66; Mismatches 116; Indels 77; Gaps 9;

QY 9 YDLICGEDSSGILSGESPECSFSDIDSSPPPTEDCYSI----- 50

Db 5 FDLICAEEDNSSI-----FDEVDN--YGVVDDVLQICNQQHGNLRNFDFTL 53

QY 51 -----ASFIEHERNFVPGFEYLSRFSRLDANAREESV 84

Db 54 ILLITIKHEHNEALISGFVANHECLASLEFEDNERQHLGLDYLRFRNGDLGARNLVI 113

QY 85 GWILKVHAYYGFOPLTAYLVNMDRFLDSRLPETNGWPLQVAVACLSLAKMEPLV 144

Db 114 DWIKVQSHYNFGLCYLVSVNYDLRFLSAELP-GKAWMQLLGVACLSLAKVDETDV 172

QY 145 PSLDLQIEGAKYIFEPRTIRRMELLYLVGLDWRLSVTPPLCLAFACKVDSTGTFFIR 204

Db 173 PLILDQVSESKFEVFEAKTIQRMELLYLVGLDWRLSVTPPLCLAFACKVDSTGTFFIR 232

QY 205 LISRAEIIIVSNIGASFLAYWPSICIAAAITLTAANEIPNMSVVK-PENAESW-CEGLRK 262

Db 233 LIFQAIQLILSTIKGIDLMFPRPSEIAAAVAISVTQQT--QIVETDKAFSFLTDHVK 289

QY 263 EKVIQCYQLMQLVINNNQKLPPLKVLPLQRLVTTRMRSSVSSSSSTSSLSLSC- 321

Db 290 ERLMKVEIMHDLRMSRSNGALASTVPSDPIGLVD--ASACLISYKSDDTSTPPSGSCG 347

QY 322 -----KRRKLN 327

Db 348 NSAHSSPASAPPPKRRKD 366

RESULT 4

C84613

probable cyclin D [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84613

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: C84613

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <STO>

A:Cross-references: GB:AE002093; NID:g4544444; PIDN:AAD22352.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g22490

A:Map position: 2

Query Match

Best Local Similarity 25.7%; Score 451; DB 2; Length 361;

Matches 120; Conservative 60; Mismatches 120; Indels 48; Gaps 9;

QY 10 DLICGEDS-SGILSGESPECSF-----SDID-----SSP---PPSPPT 44

Db 4 NLACGETSESWIIDNDNDINYGCGFTNEIDYNHQLFAKDNFGNGSTFPMGSSSSSLS 63

QY 45 EDCYSIASFIEHERNFVPGFEYLSRFSRLDANAREESVWILKVHAYYGFOPLTAYLA 104

Db 64 ED--RIKEMLVREIEFCPGTIDYVKRLISGDLDSVRNQLDWILKVCANHFGHLCICLS 121

QY 105 VNTMDRFLDSRLPETNGWPLQVAVACLSLAKMEPLVPSLIDQIEGAKYIFEPRTI 164

Db 122 MNVLDRLFTSYELPKDKMAAQLLAVSCLSLAKMEETDVPHTVDLQVEDPKFVEAKTI 181

QY 165 RRMELLYLVGLDWRLSVTPPLCLAFACKVDSTGTFFIRFLISRAEIIIVSNIGASFLA 224

Db 182 KRMELLYVTTLNWRQLALTFESFIDYVDKI--SGHVSENLIRSSRFILNTTKAIEFLD 239

QY 225 YWPSICIAAAITLTAANEIPNMSVVKPENAESWCGLRKEKYGICQYLMQELVINNNQK 284

Db 240 FRPSETIAAAAVSVSIS-GETECIDEKALSSLIYKQERVKRCLNMRSLTGEENVRG 298

QY 285 PLKVLPLQLRVTRT-----RMRSSVSSSSSSSTS 316
 DB 299 SLGQ--EQARVAVRAVPAPVGLVATCLSYRSEERTVESCTNSOSS 344

RESULT 5

51651
 cyclin delta-2 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 25-Apr-1997
 C:Accession: S51651
 R:Sonl, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Reference number: S51650
 A:Accession: S51651
 A:Molecule type: mRNA
 A:Residues: 1-383 <SON>
 A:Cross-references: EMBL:X83370
 C:Keywords: cell cycle control; cell division control

Query Match 25.38; Score 444; DB 2; Length 383;
 Best Local Similarity 35.48; Pred. No. 3.7e-32;
 Matches 115; Conservative 57; Mismatches 121; Indels 32; Gaps 7;

QY 8 DYDLGEGDSSGILSGESPECSFSDIDSSPPPTTEDCYSIASFIEHERNFVPGFYL 67
 DB 36 NHQLFRKDDNFG-GNGSIFPMGSSS-----SSLED--RIKEMLVREIEFCPTDYV 84
 QY 68 SRFGKSLDANAREESVGMILKVHAYYGFQPLTAYLVNMDRFLDSRRLPETNGWPLQL 127
 DB 85 KRLLSGDLISVRNQLDWILKCAHYHFGHLCISLNMVLDRLTSYELPKDKDWAOL 144
 QY 128 VSVACLSLAKMEPLVPSLLDQIEGAKYIEPRTIRRMELLVGLDWRLSVTPLCF 187
 DB 145 LAVSCSLASKMEETDVPPIVDQVEDPKFVEAKTIKRMELLVTTLNRLQALTPESF 204
 QY 188 LAFFACKVDSTGTFRFLISRATEIIVSNIOEASFIAWPSCTIAAAILTAANEIPNWSV 247
 DB 205 IDYFVDKI--SGHVSENLIRSSRFILNTTKAIEFLDFRSEIAAAAVSVSIS-GETEC 261
 QY 248 VKPENAESWCEGLRKEKVGICQYQMLQELVINNNQRKLDLKLVLPLQRLVTRT----- 299
 DB 262 IDEKALSLIYVKQERVKRCLNMRSLTGEENVRGTSLSQ--EQARVAVRAVPAPVGV 319
 QY 300 -----RMRSSVSSSSSSSTS 316
 DB 320 LEATCLSYRSEERTVESCTNSOSS 344

RESULT 6

T05420
 cyclin delta-3 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog; protein F28A23.80
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C:Accession: T05420; S51652
 R:Bevan, M.; Weltselgartner, M.; Fartmann, B.; Granderath, K.; Dauner, D.; Herzl, A.; N
 submitted to the Protein Sequence Database, October 1998
 A:Reference number: Z15415
 A:Accession: T05420
 A:Molecule type: DNA
 A:Residues: 1-376 <BEV>
 A:Cross-references: EMBL:AL021961
 A:Experimental source: cultivar Columbia; BAC clone F28A23
 R:Sonl, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.
 submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Reference number: S51650
 A:Accession: S51652
 A:Molecule type: mRNA

A:Residues: 1-287, 'C', 289-370, 'R', 372-376 <SON>
 A:Cross-references: EMBL:X83371; NID:9603508; PID:9603509
 C:Genetics:
 A:Map position: 4
 A:Introns: 158/3; 226/1; 269/3
 A:Note: F28A23.80
 C:Keywords: cell cycle control; cell division control

Query Match 23.78; Score 416; DB 2; Length 376;
 Best Local Similarity 32.98; Pred. No. 1.2e-29;
 Matches 105; Conservative 58; Mismatches 124; Indels 32; Gaps 5;

QY 10 DLGEGDSSGILSGESPECSFSDIDSSPPPTTEDCY-----SIASFIEHERNFVPGF 64
 DB 20 DALYCEEKWDDEGEVE-ENSSLSSSSPFVVLQDLEWEDDLVTLFSEEEQGLSCL 78
 QY 65 E--VLSRFQSRSLDANAREESVGMILKVHAYYGFQPLTAYLVNMDRFLDSRRLPETNG 122
 DB 79 DDVYLS-----TDRKEAVGMILRVNAHYGFSLAAVLAITYLDKFCISYSLQDKP 129
 QY 123 WPLQVSVACLSLAKMEPLVPSLLDQIEGAKYIEPRTIRRMELLVGLDWRLSV 182
 DB 130 WMLQVSVACLSLAKAVEEQVPLLDQVEETKYFEAKTIQRMELVLTLEWKMHLI 189
 QY 183 TPICFLAFAACKVDSTGTFRFLISRATEIIVSNIOEASFIAWPSCTIAAAILTAANEI 242
 DB 190 TPISFVDHIIRLGLKNNAHMFLNCKHRLLSVSDSRFVGYLPVVAATMMRIIEQV 249
 QY 243 PNWSVVKPENAESWCEGLRKEKVGICQYQMLQELVINNNQRKLPKLVLPQRLVTRTRMR 302
 DB 250 DPFDPISYQTNLLGLVNLTKRYKTCYDILLQLPV-----RIGLQIQIQ 294
 QY 303 SSTVSSPSSSSSTSFSLSLSC 321
 DB 295 SSKRKSHDSSSSSLNSPSC 313

RESULT 7

T45860
 cyclin D3-like protein - Arabidopsis thaliana
 N:Alternate names: protein F3A4.150
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T45860
 R:Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23007
 A:Accession: T45860
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361 <BAR>
 A:Cross-references: EMBL:AL132978
 A:Experimental source: cultivar Columbia; BAC clone F3A4
 C:Genetics:
 A:Map position: 3
 A:Introns: 157/3; 225/1; 268/3
 A:Note: F3A4.150

Query Match 23.48; Score 411; DB 2; Length 361;
 Best Local Similarity 31.48; Pred. No. 3.2e-29;
 Matches 109; Conservative 59; Mismatches 119; Indels 60; Gaps 7;

QY 6 LSDYDLGEGDSSGILSGESPECSFSDIDSSPPPTTEDCYSIASFIEHERNFVPGF 65
 DB 49 LSDHDMDDDELSTLISKQEPCLYDEI-----LDD-----E 80
 QY 66 VLSRFQSRSLDANAREESVGMILKVHAYYGFQPLTAYLVNMDRFLDSRRLPETNGWPL 125
 DB 81 FL-----VLCREKALDWIFKVKSHYGFNSLTALLAVNYDFRFTSRKFOFDKPMWS 131
 QY 126 QLVSVACLSLAKMEPLVPSLLDQIEGAKYIEPRTIRRMELLVGLDWRLSVTPPL 185
 DB 132 QLTALACLSLAKVEIRVPLLDQVEEARVFEAKTIQRMELVLTLDWRMHPVTPPI 191

QY 186 CELAFFACKVDSTGTFFIRFLISRATEIIVSNIOEASFLAYWPSCIAAAIITANEIPNW 245
 Db 192 SFFDHIIRRYFSKSHHQLEFLRCELSLLIIPDSRFLSFPVLATIMVSVIRDKMC 251
 QY 246 SVYKPENAESWCEGLRKEKVICYQLOMQLVINNNQKRLPLKVLPO---LRVTRTRM 301
 Db 252 DEAVYQSQMLTLKVDSEKYNKY---ELVLDHSPSKRMMNMWMOQSPASPIGVFASFS 307
 QY 302 RSSYVSSSSSSSTFSLS-----CKRRLN-----NRLWVD 333
 Db 308 SSSSWSVVSASASVSSSPSEPLKRRRVQEQMRLSSINRMFFD 354

RESULT 8

T49995
 cyclin protein-like - Arabidopsis thaliana
 N:Alternate names: protein F12B17.210
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49995
 R:Bevan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 225026
 A:Accession: T49995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <BEV>
 A:Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210
 A:Experimental source: cultivar Columbia; BAC clone F12B17
 C:Genetics:
 A:Gene: ATSP:F12B17.210
 A:Map position: 5
 A:Introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match 20.9%; Score 368; DB 2; Length 317;
 Best Local Similarity 35.5%; Pred. No. 2.1e-25;
 Matches 104; Conservative 47; Mismatches 104; Indels 38; Gaps 8;

QY 50 IASFEHERNFVPGFEYLSRFQSRSLDANAREESVGMILKVHAYYGFQPLTAYLVNMD 109
 Db 39 VREMIERKROHSPRDDYLRKRLNGDLDENVRIQALGWTWKACEELQFGPLCICLAMYLD 98
 QY 110 RFLDSRLPETNGWPLQVSVACLSIAKMEPLVPSLDDQIEGAKYIFEPRTIRRMEL 169
 Db 99 RFLSVHDLPSGKAMTVQLLAVACLSIAKIEETNVPELMQLQVGAPMFVEAKSVQRMEL 158
 QY 170 LVLGVLDWRLRSVTPPLCFLAFAACKVDSTGTFFIRF-LISRATEIIVSNIO----- 218
 Db 159 LVLNVLKRLKRAVTPCSYVRYPFLSKINGYDQEPHSRLVTRSLQVIASTTKGDRGLFFPK 218
 QY 219 -----EASFLAYWPSCIAAAIITANE-IPNWSYVVKPENAESWCEGLRKEKY--I 266
 Db 219 GVLIVDWAGIDFLERASEIAAVALSVSGEHFDKFSF-----SSSFSLEKERNVKKI 272
 QY 267 GCYQLMQLVINNNQKRLPLKVLPLQRLVTRTRMRSSVSSFS-SSSSTFS 318
 Db 273 G---EMIERDSSSSSSQTPNNVTYL-----QFKSRYSLSLSTASVSSSLTSL 317

RESULT 9

T09598
 cyclin 4, D-type - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09598
 R:Dahl, M.; Meskiane, I.; Boegre, L.
 Plant Cell 7, 1847-1857, 1995
 A>Title: The D-type alfalfa cyclin gene cycms4 complements G1 cyclin-deficient yeast and
 A:Reference number: Z16760; MUID:96093424
 A:Accession: T09598
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-386 <DAH>
 A:Cross-references: EMBL:X88864; NID:g1150931; PIDN:CAA61334.1; PID:g1150932
 C:Genetics:
 A:Note: cycms4

Query Match 20.9%; Score 367; DB 2; Length 386;
 Best Local Similarity 37.7%; Pred. No. 3.3e-25;
 Matches 90; Conservative 40; Mismatches 81; Indels 28; Gaps 6;

QY 52 SFIEHERNFVPGFEYLSRFQSRSLDANAREESVGMILKVHAYYGFQPLTAYLVNMDRF 111
 Db 92 TYVEDLKNVI-NEDSLQ-----PRRAVEWMLKVNAHYGFSALTATLVAVNYLDRF 141
 QY 112 LDSRRLPETNGWPLQVSVACLSIAKMEPLVPSLDDQIEGAKYIFEPRTIRRMELV 171
 Db 142 LLSFHQKEKPMIQLVAVTCISIAKVEETQVPLLDLQVQDTKYVEAKTIQRMELI 201
 QY 172 LGVLDWRLRSVTPPLCFLAFA---FACKVDSTGTFFIRFLISRATEIIVSNIOEASFLAYW 227
 Db 202 LSTLKWMHPVTHSFIDHTRRLGLKTNLHMEFLR---RCENLLSVLLDSRFVGCVP 257
 QY 228 SCIAAAIITANEIPNWSYVVKPENAESWCEGL-----RKEKVICYQLOMQLVINNN 280
 Db 258 SVLATATMLHVIDQIEQ---SDDNGVDYKQNLVNLKISKEVDECTYNAIHLTNANN 312

RESULT 10

E85041
 probable D-type cyclin [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: E85041
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold SP
 Nature 402, 769-777, 1999
 A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488
 A:Accession: E85041
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <STO>
 A:Cross-references: GB:NC_001268; NID:g7270197; PIDN:CAB77812.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4g03270
 A:Map position: 4

Query Match 19.4%; Score 340.5; DB 2; Length 302;
 Best Local Similarity 33.25%; Pred. No. 5.9e-23;
 Matches 93; Conservative 54; Mismatches 106; Indels 33; Gaps 9;

QY 57 ERNFVPGFEYLSRFQSRSLDANAREESVGMILKVHAYYGFQPLTAYLVNMDRFLDSRR 116
 Db 35 EFQHPSSHYFHSLSKSAFLSNRQAISITQYSKFD-DPSLTLYAVNYIDRFLSSED 93
 QY 117 LPETNGWPLQVSVACLSIAKMEPLVPSLDDQIEGAKYIFEPRTIRRMELVGLVD 176
 Db 94 MPQSKPWILKILISLSCVSLSAKMRKPPDM-SVSDLPVEGE--FFDAQMIERNENVILGALK 150
 QY 177 WRLRSVTPPLCFLAFA---FACKVDSTGTFFIRFLISRATEIIVSNIOEASFLAYWPSCIAA 232
 Db 151 WRMRSVTPPSFLAFISLFLKEDPDLKHSLSQTSGLTFSLQHDISFLFKPSVIAG 210
 QY 233 AAILTANET-----PNMSYVVKPENAESWCEGLRKEKVICYQLOMQLVINNNQKRLP 285
 Db 211 AAILFASFECLPQPCFS-----NRINQCTYVNMKDELMCKYKAIQERDIYGENGS-- 263
 QY 286 LKVLPLQRLVTRTRMRSSVSSSSSTFS--SLSGKRRKLNNR 329
 Db 264 -----TETAVNVLDQGFSSGCSGSDKSTITTAASSSRKRRTSTR 300

RESULT 11

T04720
 hypothetical protein F19F18.120 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04720
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
Submitted to the Protein Sequence Database, March 1999
A:Reference number: 215382
A:Accession: T04720
A:Molecule type: DNA
A:Residues: 1-321 <BEV>
A:Cross-references: EMBL:AL035605
A:Experimental source: cultivar Columbia; BAC clone F19F18
C:Genetics:
A:Map position: 4
A:Introns: 83/1; 112/1; 212/1; 261/3
A:Note: F19F18.120

Query Match 15.7%; Score 276; DB 2; Length 321;
Best Local Similarity 26.3%; Pred. No. 4.2e-17;
Matches 84; Conservative 59; Mismatches 144; Indels 32; Gaps 9;

QY 12 LCGDSSGILSGESPECSFSDIDSSPPPTPTEDCYSTASIEHERNTPGFEYLSRFQ 71
Db 12 LCHSESSL--NEDDETERSDKQEPHTTTIDDEDYADLVLEN-----LRF 60
QY 72 --SRSLDANAREESGVILKVHAYYGQPLTAYLVAVNMDRFLDSRLPBTNGWPLQV 128
Db 61 TLPSKTTSSDRLLADWLTWHKKNKPTNSLHCHNLIRSVSPKIHREYEWAMRL 120
QY 129 SVACLSLAKMEEPVPSLLDQIEGAKYIEPRTIRRMELVLGVDWRLRSVTPCLFL 188
Db 121 SVACLSLAKMEERIVPGLSQYP-QDHDFVFKPDVIRKTELLISTLDWKMNLTPPHYF 179
QY 189 AFAACKV--DSTGTFLRLISRATEIIVSNIOEASFVAYWPSCIAAAILTAAN----- 240
Db 180 NYFLAKISODNHSVKDLVLRSSDSLALTKELISFTEYRQVVAATVTLASSSTSDI 239
QY 241 EIPNWSVVKPENAESWCEGLRKEKVICGYQLMQLVINNNQKRLPLKVLPLQVTRTR 300
Db 240 RLTRBEIANKFGSISWTSNENNVLYCYQ-RTLEIEERKHTP----PPEIAVSREPP 293
QY 301 MRSSTVS--SFSSSSSTS 316
Db 294 ASGSGAKRRLSFDDSDQS 312

RESULT 12
A96803
probable mitotic cyclin a2-type [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: A96803
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khah, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: A96803
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <STO>
A:Cross-references: GB:AE05173; NID:g11079479; PIDN:AAG29191.1; GSPDB:GN00141
C:Genetics:
A:Gene: P2P24.10
A:Map position: 1
C:Superfamily: cyclin

Query Match 14.1%; Score 247; DB 2; Length 454;

Best Local Similarity 28.6%; Pred. No. 2.7e-14;
Matches 106; Conservative 48; Mismatches 128; Indels 88; Gaps 18;

QY 8 DYDLGGEBSGILSGESPECSFSDIDSSPPPTPTEDCYSTASIEHERNTPGFEYLSRFQ 46
Db 102 DTELLQSDDS---LLCSSPALS---LDASPTQSDPSISTHDSLTHNVVDYVVESTTDDGN 155
QY 47 -----CYSTASFI-EH-----ERNFVPGFEYLSRFQSRSLDANAREE 82
Db 156 DDDDEIVNIDSLMDPOLCASACDIYEHLYRSEYVNRKRPALDYMERQOS-SINAMRSI 214
QY 83 SVGWILKVHAYYGQPLTAYLVAVNMDRFLDSRLPBTNGWPLQVSVACLSLAKMEEP 142
Db 215 LIDWLVEVAEEYRLSPETLYLVAVNVDRLTGNAINKON--LQILGVTGCMIAAKYEEV 271
QY 143 LVPSLLDQIEGAKYIEPRTIR--RMELVLGVDWRLRSVTPCLFLAFAACKVDST 198
Db 272 CVP-----QVEDFCYITDNTYLRNLELMESSVLYNLFELTTPFAKCFRLRAAQR 326
QY 199 GTFIRFLISRATEIIVSNIOEAS-----FLAYWPSCIAAAILTAANEI-PNWSVVKPEN 252
Db 327 ---KEVPSLSECLACYLTEELSLDYAMLRYAPSLVAASAVFLAQYTLHPS---RKPN 379
QY 253 AE-SWCEGLRKEKVICGYQLMQLVINNNQKRLPLKVLPLQVTRTRRSSTV-----S 307
Db 380 ATLEHYTSYAKHMEACVKNLQLC---NEK---LSSDVVAIRKWTSLQORSFVPRHYRK 433
QY 308 SFSSSSSTSF 317
Db 434 SFSSDSVSGY 443

RESULT 13
T48232
hypothetical protein T7H20.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48232
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
Submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24488
A:Accession: T48232
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <BEV>
A:Cross-references: EMBL:AL162508
A:Experimental source: cultivar Columbia; BAC clone T7H20
C:Genetics:
A:Map position: 5
A:Introns: 87/3; 116/3; 215/1
A:Note: T7H20.160

Query Match 13.9%; Score 244; DB 2; Length 341;
Best Local Similarity 26.6%; Pred. No. 3.5e-14;
Matches 76; Conservative 56; Mismatches 128; Indels 26; Gaps 8;

QY 10 DLGGEBSGILSGESPECSFSDIDSS-----PPPSPTPTEDCYSTASIEHERNTPGFEYLSRFQ 61
Db 3 NLCEESWPASPFLTPPELPNFRHRSHDNDVVKMYEIDAATMEE--AIAMDLEKELCFNN 60
QY 62 PGFEYLSRFQSRSLDANAREESGVILKVHAYYGQPLTAYLVAVNMDRFLDSRLPBTNG 121
Db 61 HGDKFEVEFVSKRL-TDYRFHARQWLITRSRLNLSYETVFAANCFDRFVMTCCDEWT 119
QY 122 GWPLOVSVACLSLAKMEEPVPSLLDQIEGAKYIEPRTIRRMELVLGVDWRLRS 181
Db 120 NMVVELVAVTSLSASKFNEVTPDLELEMEGLTHMFHVNTVAQMEELILKALEWYVA 179
QY 182 VTPICFLAFAACKVDSTGTGTFLRLISRATEIIVSNIOEASFVAYWPSCIAAAILTAANE 241
Db 180 VTSYTFSGTLVSKIGMGD--HMIIMRITNHLIDVYCDLKMQLQYPPSVAVATAAI----- 231
QY 242 IPNWSVVKP---ENAESWCEGLRKEKVICGYQLMQLVINNNQKRLPLKVLPLQVTRTR 300

DB 232 ---WILMEDKVCRESIMNLFEDNHKEIKVCVDGMKRDIDHSSR 274

RESULT 14

T02746
cyclin A-like protein CYCZM2W - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999
C:Accession: T02746

R:Histoh. W.L.; Wolniak, S.M.
Plant Mol. Biol. 37, 121-129, 1998
A:Title: Isolation and characterization of a functional A-type cyclin from maize.
A:Reference number: 214713; MUID:98281580

A:Accession: T02746
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-502 <HS1>
A:Cross-references: EMBL:U50064; NID:g1399509; PIDN:AAC50013.1; PID:g1399510

A:Experimental source: cultivar Merit; root tip

C:Genetics:

A:Gene: CYCZM2W

C:Superfamily: cyclin

Query Match 13.0%; Score 228; DB 2; Length 502;

Best Local Similarity 29.2%; Pred. No. 1.6e-12;

Matches 77; Conservative 42; Mismatches 103; Indels 42; Gaps 10;

QY 29 SFSDIDSPPTPTEDCYSIASF-----EHERNFVPGFEYLSRFQSRSLDANAREES 83

DB 217 SICEVDSNFEDP-----QLCALASDIYHMLREAEKKRPSTDFMETIQ-KDVNPSMRAIL 271

QY 84 VGMILKVHAYYGQPLTAYLVANVMDRFLDSRRLPETNGWPLQLVSVACLSIAKMEEP 143

DB 272 IDWLEVAEEYRLAPDTLYLVNYIDRLSGN---EINRQRLQLGVACMLIAKYEIC 328

QY 144 VPSLLDQIEGAKYIEPRTIR---RMELLVGLVDWRLRSVTPICFLAF-----ACK 194

DB 329 AP-----QVEEFCYITDNTYFRDEVLEMEASVLNLYLKFEWTAPTAKCFLRFRFARSAQACD 383

QY 195 VDSGTGFIIRFLISRATETIVSNIOEASFLAYWPSCIAAAAILTAA-----NEIP 243

DB 384 ED-PALHLEFLANYIAEL---SLEYSLSLSPPSLIAASAIFLARFVLQPTKYPWNSTLA 439

QY 244 NMSVVKPENAESWCEGLRKEKVG 267

DB 440 HYTOYKPSSELSECVKALHRLSSVG 463

RESULT 15

C57742

cyclin II - maize

C:Species: Zea mays (maize)

C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 16-Jul-1999

C:Accession: C57742

R:Renaudin, J.P.; Colasanti, J.; Rime, H.; Yuan, Z.; Sundaresan, V.

Proc. Natl. Acad. Sci. U.S.A. 91, 7375-7379, 1994

A:Title: Cloning of four cyclins from maize indicates that higher plants have three stru

A:Reference number: A57742; MUID:94316698

A:Accession: C57742

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-456 <REN>

A:Cross-references: GB:U10076; GB:U10077; NID:g516549; PIDN:AAA20237.1; PID:g516550; GB:

C:Superfamily: cyclin

Query Match 12.5%; Score 220; DB 2; Length 456;

Best Local Similarity 27.7%; Pred. No. 7.5e-12;

Matches 78; Conservative 44; Mismatches 106; Indels 54; Gaps 11;

QY 32 DIDSGPPSPPTEDCYSIASF-----EHERNFVPGFEYLSRFQSRSLDANAREESYGW 86

DB 171 DVDSEYEDP-----QLCATLASDIYHMLREAEETKRPSTDFMEMIQ-KDVNPSMRAILIDW 225

QY 87 ILKVHAYYGQPLTAYLVANVMDRFLDSRRLPETNGWPLQLVSVACLSIAKMEEPVPS 146

DB 226 LVEVAEEYRLVDPDTLYLVNYIDRLSGNEIRRRK---LQLGVACMLIAKYEICAP- 281

QY 147 LLDLQIEGAKYIEPRTIR---RMELLVGLVDWRLRSVTPICFLAF-----ACKYDS 197

DB 282 ---QVEEFCYITDNTYFRDEVLEMEASVLNLYLKFEWTAPTAKCFLRFRFARAAQACED- 336

QY 198 TGTFIIRFLISRATETIVSNIOEASFLAYWPSCIAAAAILTAA-----NEIPNWS 246

DB 337 PALHLEFLANYIAEL---SLEYSLSLSPPSLIAASAIFLARFVLQPTKYPWNSTLAHYT 393

QY 247 VVKPENAESWCEGLRKEKVG 288

DB 394 QYK-----SKLSECVKALHRLCSVSGSGLNLPALR 423

Search completed: October 23, 2002, 14:39:31
Job time : 19 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:34:34 ; Search time 14 Seconds
(without alignments)
937.566 Million cell updates/sec

Title: US-09-665-308D-12
Perfect score: 1758
Sequence: 1 MSVSCLSDYDLGCGEDSSGI.....SCKRRKLNRLWVDKGNSE 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	57.8	335	1 CGD1_ARATH	P42751 arabidopsis
2	451	25.7	361	1 CGD2_ARATH	P42752 arabidopsis
3	417	23.7	376	1 CGD3_ARATH	P42753 arabidopsis
4	205.5	11.7	441	1 CG22_ANTMA	P34801 antirrhinum
5	201	11.4	328	1 CGB2_MESAU	P37883 mesocricetu
6	200	11.4	328	1 CG2B_MEDSA	P30278 mesocricetu
7	200	11.4	434	1 CG2B_MEDVA	P46278 medicago sa
8	199	11.3	428	1 CG2B_ARATH	P30183 arabidopsis
9	198.5	11.3	491	1 CG22_YEAST	P24869 saccharomyc
10	197.5	11.2	454	1 CG21_SOYBN	P25011 glycine max
11	196.5	11.2	341	1 CG2A_DAUCA	P25010 daucus caro
12	196.5	11.2	419	1 CG2B_ORYSA	P40671 oryza sativ
13	196.5	11.2	471	1 CG21_YEAST	P24868 saccharomyc
14	196	11.1	398	1 CGB2_HUMAN	P35067 homo sapien
15	194.5	11.1	473	1 CG21_ANTMA	P47827 xenopus lae
16	191.5	10.9	415	1 CGA2_XENLA	P47827 xenopus lae
17	190	10.8	398	1 CGB2_MOUSE	P30276 mus musculu
18	190	10.8	399	1 CGB2_CHICK	P29332 gallus gall
19	189.5	10.8	408	1 CG2B_MEDVA	P24862 patella vul
20	189	10.8	428	1 CG1B_MEDVA	P46277 medicago va
21	188.5	10.7	426	1 CG2A_PATVU	P24861 patella vul
22	187.5	10.7	291	1 CGD1_BRARE	P30459 brachydanio
23	187	10.6	398	1 CGB2_BOVIN	P25012 bos taurus
24	185.5	10.6	257	1 CG22_SOYBN	P25012 glycine max
25	184.5	10.5	430	1 CGB1_MOUSE	P24860 mus musculu
26	183	10.4	291	1 CGD2_XENLA	P33782 xenopus lae
27	182.5	10.4	432	1 CGA2_MOUSE	P51943 mus musculu
28	182.5	10.4	432	1 CGA2_HUMAN	P20248 homo sapien
29	181.5	10.3	406	1 CGA2_BOVIN	P30274 bos taurus
30	180.5	10.3	409	1 CG2B_ARBPB	P07818 arabacia pun
31	180.5	10.3	423	1 CGB1_RAT	P30277 rattus norv
32	180	10.2	397	1 CGB1_XENLA	P13350 xenopus lae
33	179.5	10.2	291	1 CGD1_XENLA	P50755 xenopus lae

34	179.5	10.2	392	1 CGB2_XENLA	P13351 xenopus lae
35	179	10.2	395	1 CGA2_CHICK	P43449 gallus gall
36	178.5	10.2	289	1 CGD2_MOUSE	P30280 mus musculu
37	177.5	10.1	288	1 CGD2_RAT	P04827 rattus norv
38	177.5	10.1	421	1 CGA2_MESAU	P37881 mesocricetu
39	176.5	10.0	289	1 CGD2_HUMAN	P30279 homo sapien
40	176.5	10.0	482	1 CG23_SCHPO	P10815 schizosacch
41	176	10.0	421	1 CGA1_MOUSE	P61456 mus musculu
42	175	10.0	295	1 CGD1_RAT	P39948 rattus norv
43	175	10.0	420	1 CG2A_CHIVR	P51986 chlorohydra
44	174.5	9.9	380	1 CGS6_YEAST	P32943 saccharomyc
45	174.5	9.9	429	1 CGB1_CRILLO	P08301 cricetus

ALIGNMENTS

RESULT 1
ID CGD1_ARATH STANDARD; PRT; 335 AA.
AC P42751; 004525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cyclin delta-1.
GN CYCD1 OR AT1G70210 OR F20P5.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. LANDSBERG RECTA; TISSUE=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif."
RL Plant Cell 7:85-103(1995).
RN [2]
RP REVISIONS.
RA Murray J.A.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Millscher J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shin P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. LANDSBERG ERECTA; TISSUE=Seedling;
 RX MEDLINE=95210930; PubMed=7696881;
 RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
 RT "A family of cyclin D homologs from plants differentially controlled
 RT by growth regulators and containing the conserved retinoblastoma
 RT protein interaction motif.";
 RL Plant Cell 7:85-103(1995).
 RP [2]
 RP REVISION TO 371.
 RA Murray J.A.H.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
 RA Kreis M., Delsený M., Pulgomech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weljens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Wetzenecker T., Bothé G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirksé W.,
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Benneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyshaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail A., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlroy K., Mayes R.,
 RA Petrelet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fatmann B., Granderath K., Dauner P., Herzl A.,
 RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chetoui F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Blatke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheel P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kallicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., All J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodihi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:769-777(1999).
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

[illegible]

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; X76123; CAA53729.1; -
DR PIR; S41710; S41710.
DR HSSP; P20248; 1FIN.
DR InterPro; IPR000553; Cyclin.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; cell cycle; Cell division; Mitosis.
SQ SEQUENCE 441 AA; 49205 MW; E6E4C037C98880A7 CRC64;

Query Match 11.7%; Score 205.5; DB 1; Length 441;
Best Local Similarity 27.2%; Pred. No. 2.6e-11;
Matches 74; Conservative 51; Mismatches 112; Indels 35; Gaps 12;

QY 26 PECSFSDIDSSPPPTTEDCYSIASFIEHERNFVPGFEYLSR--FQSRSLDANAREE 82
Db 168 PKEQIVDIDAA-----DVNNDLAVEVEYEDMYKFKSAENDSRPHYMDSQPEINEKMR 221
QY 83 S--VGWILKHAHYVGFOPLTAYLAVNVMDRFLDSRRLPETNGWPLQLVSVACLSLAKME 140
Db 222 AILIDWLVOYHYKFKELSPETLYLTINIVRYLASK---TTSRRELQLGMSMLIASKYE 278
QY 141 EPLVPSLLDIO-IEGAKYIEPRTIRRMELVLGVLDWRLRSVTPLCFLAF--ACKVDS 197
Db 279 EIWAPEVNDLVCTISDGSYSNE--QVLRMKKILGALWYLTVPYFVLYRFIKASLPDS 336
QY 198 --TGTFFRLISRATEIIVSNIQEASFAYWPSCIAAAAILTA--ANEIPNWSVVKPEN 252
Db 337 DVEKNMVYFL----AELGMNMY--ATTIMYCPSMIAAAVYAARCTLNKMPIMNETLRMH 390
QY 253 AESWCEGLRKEKVIQCYQLMOELVINNNQRL 284
Db 391 T-----GFSEVQLMDCAKLLIDFHGSTDQKL 417

RESULT 5
CGB2_MESAU STANDARD; PRT; 397 AA.

ID CGB2_MESAU STANDARD; PRT; 397 AA.
AC P37883;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin B2.
GN CCNB2.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Shiraki T., Yamashita K., Nishitani H., Nishimoto T.;
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; D17294; BAA04127.1; -
DR HSSP; P20248; 1JSU.
DR InterPro; IPR000553; Cyclin.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; cell cycle; Cell division; Mitosis.
SQ SEQUENCE 397 AA; 45278 MW; 247DBAA412E6CBBD CRC64;

Query Match 11.4%; Score 201; DB 1; Length 397;
Best Local Similarity 25.4%; Pred. No. 5.9e-11;
Matches 81; Conservative 54; Mismatches 134; Indels 50; Gaps 12;

QY 12 LCGEDSSGILSGESPESFSDIDS---SPPPPPTTEDCYSIASFIEHERNFVPGFEYL 67
Db 104 LQAFSDAL-----CKIEDIDNEDWENPOLCSDYKDIYQLRLQLEVLSINPHF--- 154
QY 68 SRFQSRSLDANAREESVWILKVHAYVGFOPLTAYLAVNVMDRFLDSRRLPETNGWPLQL 127
Db 155 --LDGRDINGRMRAILVDLVQVHSHKFRLLQETLLYMCIAIMDRFLQADQVCRKK---LQL 209
QY 128 VSVACLSLAAKMEELVPSLLDQIEGAKYI---EFPRTIRRMELVLGVLDWRLRSVT 183
Db 210 VGITALLASKYEEMRSPN-----IEDFVYITDNAVYSSQIREMETLILKEIKFELGRPL 264
QY 184 PLCEL--AFFACKVD-STGTFFRLISRATEIIVSNIQEASFAYWPSCIAAAAILTAAN 240
Db 265 PLHFLRRASKAGEVDVQHTLAKYLME-----LTLIDYDMVHYHPSQVAAAASCLSQK 317
QY 241 EI--PNWSVVKPENAESWCEGLRKEKVIQCYQLMOELVINNNQRLPLKVLPO----- 292
Db 318 VLQGGKWNL-----KQYYTGYMETEVLEVQMHAKNVYKVNENLTKFIAVKNKYASSRL 372
QY 293 LRVYTRTRMRSSVVSFSFS 311
Db 373 LKSTIPQLNSKITKDIAS 391

RESULT 6
CGB2_MEDSA STANDARD; PRT; 328 AA.

ID CGB2_MEDSA STANDARD; PRT; 328 AA.
AC P30278;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycms2) (Fragment).
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93104677; PubMed=1307238;
RA Hirt H., Mink M., Pfosser M., Boegre L., Gyorgyey J., Jonak C.,
RA Gartner A., Dudits D., Hebelde-Bors E.;
RT "Alfalfa cyclins: differential expression during the cell cycle and
RT in plant organs.";
RL plant Cell 4:1531-1538(1992).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS

Query Match	11.48;	Score 200;	DB 1;	Length 328;
Best Local Similarity	26.68;	Pred. No. 5.6e-11;		
Matches 67;	Conservative 41;	Mismatches 112;	Indels 32;	Gaps 9;
QY 32	DIDSSPPSPPTTDCYSIASFIEHERNFVPGFEYLS----	RFQSRSLDANAREES--	VG 85	
Db 55	DIDSC-----	DANSLAVVEYIEDLHAYYRKIEYLGCVSPTYMDEQLDINERMALIVD	108	
QY 86	WILKVHAYYGQPLPAVLAVNYMDRFLDSRRLPETNGWPLQIVSVACLSLAKMEEP	LYP 145		
Db 109	WLIEVHDKFDLMQETLELTVNLIDRFLAKQNVRRK---	LQVLGVAMLLACKYEESVP 165		
QY 146	SLLDLIQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSTYPLCLAF--	ACKVDSTGTFIR 203		
Db 166	VVSDL-IHIADRAVTRKDLILEMEKMLNTLQYNSLPTAVYVFMRRFLKAAQADKKLELVA	224		
QY 204	FLISRATEIIVSNIOEASFLAYWPSCIAAAAILTA---ANEIPNWSVVKPENAESWCEGL	260		
Db 225	FF-----LVDLISLVEYEMLKFPSPSLVAAAAYTAQCTVSGEKKHMN----	KTCENHTNY 273		
QY 261	RKEKVICGYOLM 272			
Db 274	SEDQLLECSMLM 285			

RESULT 7	CG2B_MEDVA	STANDARD;	PRT;	434 AA.
ID	CG2B_MEDVA			
AC	P46278;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycms2).			
OS	Medicago varia.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.			
OX	NCBI_TaxID=36902;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. A2;			
RX	MEDLINE=95375541; PubMed=7647566;			
RA	Meskiene I., Boegre L., Dahl M., Plick M., Ha D.T.C., Swoboda I.,			
RT	Heberle-Bors E., Ammerer G., Hirt H.;			
RT	"cycms2, a novel B-type alfalfa cyclin gene, is induced in the			
RT	G0-to-G1 transition of the cell cycle.";			

RL Plant Cell 7:759-771(1995).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION.
 CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
 CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
 CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
 CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X82040; CAA57560.1; -.
 DR HSSP: P20248; 1FIN.
 DR InterPro: IPR000553; Cyclin.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN; 2.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR Cyclin; Cell cycle; Cell division; Mitosis.
 KW SEQUENCE 434 AA; 49367 MW; 644EFOA2681A4C32 CRC64;
 SQ

Query Match	11.4%;	Score 200;	DB 1;	Length 434;
Best Local Similarity	26.6%;	Pred. No. 8.3e-11;		
Matches	67;	Conservative 41;	Mismatches 112;	Indels 32; Gaps 9;
QY	32	DIDSSPPPTTEDCVSIASFIHERNFVPGFEYLS----	RFQSRSLDANAREES--VG	85
			: : : :	:
Db	161	DIDSC-----DANSLAVEVEIEDLHAYRKIEYLCVSPTYMDEQLDINERMALIVD		214
QY	86	WILKVHAYYGQPLFAYLAVNYMDRFLDSRRLPETNGMPQLQVSVACLSLAKMEEP		145
		:: :	: : :	:
Db	215	WLIEVHDKFDLMQETLEFLTVNLIDRFLLAKQNVRRK---LQVLGVAMLLACKYEEVS		271
QY	146	SLLDLQIEGAKYIFEDRTIRRMELLVLGVLDWRLRSVTPLCFLAF--ACKVDSJGT		203
		: :	: : :	: : : :
Db	272	VVSDL-IHIADRAYTRKDLIEMEKMLNTLQYNMSLPTAYVFMRRFLKAAQADKKLELVA		330
QY	204	FLISRATEIIVSNIOEASFLAYWPSCIAAAAILTA---ANEIPNWSVVKPENAESNCEGL		260
		: : : :	: : : :	: :
Db	331	FF-----LVDSLVEYEMLKFPPLVAAAAYTAOCTVSGFKHMN-----KTCENHTNY		379
QY	261	RKEKVIGCYQLM		272
		: : : :		
Db	380	SEDQLLECSMLM		391

RESULT 8			
	CG2B_ARATH		
ID	CG2B_ARATH	STANDARD;	PRT; 428 AA.
AC	P30183; Q42081;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	G2/mitotic-specific cyclin (B-like cyclin).		
GN	CYCL1 OR AT4G37490 OR F6G17.140.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CV. C24;		
RX	MEDLINE=92228771; PubMed=1373494;		
VA	Hemerly A.S., Bergounioux C., van Montagu M., Inze D		

RA Ferreira P.C.G.;
RT "Genes regulating the plant cell cycle: isolation of a mitotic-like
RT cyclin from Arabidopsis thaliana."
RL Proc. Natl. Acad. Sci. U.S.A. 89:3295-3299(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansoerge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohensei J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E.,
RA Welteneegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetler P.,
RA Bernseiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIlay K., Mayes R.,
RA Pettelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirliou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj P., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threiden J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney J., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante S., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vll D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hofman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martenssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
RN [3]
RP SEQUENCE OF 6-94 FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Phillips G., Gigot C.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; M80190; AAA32781.1; -
DR EMBL; X62279; CAA44169.1; -
DR EMBL; AL035601; CAB38216.1; -
DR EMBL; AL161591; CAB80414.1; -
DR EMBL; Z26397; CAA81236.1; -
DR PIR; A44123; A44123.
DR HSSP; P20248; 1JSU.
DR InterPro; IPR000553; Cyclin.
DR Pfam; PF00134; cyclin_C; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Mitosis.
KW CONFLICT 91 K -> N (IN REF. 1).
FT
SQ SEQUENCE 428 AA; 48459 MW; 83334927768D8857 CRC64;

Query Match 11.3%; Score 199; DB 1; Length 428;
Best Local Similarity 26.9%; Pred. No. 1e-10;
Matches 63; Conservative 45; Mismatches 100; Indels 26; Gaps 8;

QY 45 EDCYSIASFIEHE--RNFVPGFEYLSRFQSRSLDANARESYGWLKVHAYYGFOPLTA 101
Db 167 EDIYSFYKSVSESEWRPRDYMA-----SQPDINEKMRLLIYEWLIDVHVFELNPETF 218

QY 102 YLAVNMDRFLDSRRLPETNGWPIQLVSVACLSLAAKMEPLVPSLLDLQIEGAKYIFEP 161
Db 219 YLTVNIDRFLSVKVPVRKE--LQVLGLSALLMSAKYEELWPRQYEDL-VDIADHAYSH 274

QY 162 RTIRRMELVLVGLDWRLRSVTPPLCFIAFFACKVDSTGTFIRFLISRATETIVSNIQEAS 221
Db 275 KQILVMEKTLILSTLEWYLTVPHTHYELARF-IKASIADEKEMENVHYLAELGVMHYD--T 331

QY 222 FLAYWPSCIAAAAILTAAN--EIPNMSVYKPENAESWCCEGLRREKVIQCYQLM 272
Db 332 MIMFSPMVAASAIIYAARSSLRQVPITWSTLKHHT----GYSETQLMDCAKLL 380

RESULT 9
CG22_YEAST STANDARD; PRT; 491 AA.
ID CG22_YEAST
AC P24869;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE G2/mitotic-specific cyclin 2.
GN CLB2 OR YPR119W OR P9642.6.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91191554; PubMed=1849457;
RA Surana U., Robitsch H., Price C., Schuster T., Fitch I., Fitch A.B.,
RA Nasmyth K.;
RT "The role of CDC28 and cyclins during mitosis in the budding yeast S.
RT cerevisiae."
RL Cell 65:145-161(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=93051323; PubMed=1427070;
RA Richardson H., Lew D.J., Henze M., Sugimoto K., Reed S.I.;
RT "Cyclin-B homologs in Saccharomyces cerevisiae function in S phase
RT and in G2."
RL Genes Dev. 6:2021-2034(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Talch A., Trevaskis E., Vignati D.,
RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 PROTEIN KINASE TO
CC FORM MPF. G2/M CYCLIN ACCUMULATE STEADILY DURING G2 AND ARE
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED BEFORE MITOSIS. THE
CC LEVELS PEAK LATE IN THE G2 PHASE OF THE CELL CYCLE AND ARE AT A
CC MINIMUM IN G1 PHASE.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M65070; AAA34502.1; -
DR EMBL; X62319; CAA44195.1; -
DR EMBL; U40828; AAB68060.1; -
DR PIR; S14166; S14166.
DR HSSP; P20248; IJ5U.
DR SGD; S0006323; CLB2.
DR InterPro; IPR000553; Cyclin.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLIN; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis; Multigene family.
SQ SEQUENCE 491 AA; 56246 MW; B68FF88871022A0 CRC64;

Query Match 11.3%; Score 198.5; DB 1; Length 491;
Best local Similarity 25.5%; Pred. No. 1.3e-10;
Matches 84; Conservative 59; Mismatches 119; Indels 67; Gaps 18;
QY 3 VSCLSYDL-----LCGEDSSGILSGESPSFSDIDSSPPSPPTEDCYSIASFIHE 57
DB 187 ISTIVEQELPKRKVCDENG-----KEEYEMEDLDAE-----DVNDPEMVSEYV--- 230
QY 58 RNFVPGFEYLSR-----FQSRSLDANARESVGMILKVHAYYGFQPLTAYLAV 105
DB 231 -NDI--FEYLHOLEVITLPKKEEDLYQHRNHNHON-RDILVNMVLKIHNFGLLPETLYLAI 286
QY 106 NYMDRFLDSRLPETNGWPLQLVSVACLSLAAMEEPLVPSLIDLQIEGAKYIEPRTIR 165
DB 287 NIMDRFL-GKELVQLD--KLQLVGTSCLFLASKYEYVSPSIKHFASCTDE-IK 342
QY 166 RMELVLGLVLDWRLRSVTPICFLAFAACKVD---STGTFFIRFLISRATFIIVSNIQAS 221
DB 343 EGEKFLKTLKFNLMYPNPNNFLRIS-KADDYDIQSRTLAKFL---RI---SLVDFR 394
QY 222 FLAYWPSCIAAAAILTAANEI--PNMSVVKPENAESWCEGLRKEKVIK-CYQLMQELVIN 278
DB 395 FIGILPSICAAAMFMSRKMLGKGWD-----GNLIHYSGGYTKKEELAPYCHMINDYLV-- 448
QY 279 NNQKRLPLKLVLPOLRVTTTRTRMSSTVS 307
DB 449 -----SPTVHDEHRRKYQSRFMKASIS 472

RESULT 10
CG21_SOYBN STANDARD; PRT; 454 AA.
ID CG21_SOYBN
AC P25011;
DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin S13-6 (B-like cyclin).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. AKISENGOKU; TISSUE=Root;
RX MEDLINE=91330894; PubMed=1831125;
RA Hata S., Kouchi H., Suzuki I., Ishii T.;
RT "Isolation and characterization of cDNA clones for plant cyclins.";
RL EMBO J. 10:2681-2688(1991).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62820; CAA44632.1; -
DR PIR; S16522; S16522.
DR HSSP; P30274; IVIN.
DR InterPro; IPR000553; Cyclin.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLIN; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 454 AA; 50094 MW; 54EB4596586A7C10 CRC64;

Query Match 11.2%; Score 197.5; DB 1; Length 454;
Best local Similarity 25.9%; Pred. No. 1.5e-10;
Matches 69; Conservative 45; Mismatches 103; Indels 49; Gaps 11;
QY 26 PECFSFSDIDSSPPPPSPTT---EDCYSIASFIHERNFVPGFEYLSRFQSRSLDANARE 81
DB 173 PKEQIIDIDASDVNDNELAAVEYIDYIKFYKLVENESR--PHDYIG--SQPEINERARA 227
QY 82 ESVGWILKVHAYYGFQPLTAYLAVNMDRFLDSRLPETNGWPLQLVSVACLSLAAMEE 141
DB 228 ILVDWLIDVHTKFLSLTLYLTINIDRFLAVKTVPRRE---LQLVGISAMLSKYE 284
QY 142 PLVPSLUD-LQIEGAKYIEPRTIRRMELVLVGLDWRLRSVTPICFLAFAACKVDSTGT 200
DB 285 IMPPEVNDPEVCLSDRAYTHE--HILTMKTLINKLEWTLTVPPPLVFL----- 330
QY 201 FIRFLISRATFIIVSNIQASFLA-----YWPSCIAAAAILTA--ANEIPNMS 246
DB 331 -VRFIKASVDQELDNM--AHFLSELGMNMYATLMYCPMSVAASAVLAARCTLNKAPFN 387
QY 247 VVKPENAESWCEGLRKEKVIKGYQLM 272
DB 388 ETLKLT-----GYSQQLMDCARLL 408

RESULT 11
CG2A_DAUCA STANDARD; PRT; 341 AA.
ID CG2A_DAUCA
AC P25010;
DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE G2/mitotic-specific cyclin C13-1 (A-like cyclin) (Fragment).
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. KURODAGOSUN;
RX MEDLINE=91330894; PubMed=1831125;
RA Hata S., Kouchi H., Suzuki I., Ishii T.;
RT "Isolation and characterization of cDNA clones for plant cyclins.";
RL EMO J. 10:2681-2688(1991).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
(MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
CC KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62819; CAA44631.1; -.
DR PIR; S16521; S16521.
DR HSSP; P20248; IJSU.
DR InterPro: IPR000553; Cyclin.
DR Pfam; PF00134; cyclin_1.
DR SMART; SM00384; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
FT NON_TER 1
SQ SEQUENCE 341 AA; 38724 MW; 5708DF4269C06F3F CRC64;

Query Match 11.2%; Score 196.5; DB 1; Length 341;
Best Local Similarity 26.4%; Pred. No. 1.3e-10;
Matches 77; Conservative 44; Mismatches 122; Indels 49; Gaps 11;

QY 10 DLTCGDDSSGILSGESPEC-----SFSDIDSSPPPTTEDCYSIASF 53
DB 32 DLTCRE-----FEVPCVAAQKKRRKGVKEDGVDFGEKFDPMCSAYVSDVYEYTKQ 84

QY 54 IEHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLD 113
DB 85 MEMETKRPMNNYIEQVQ-KDVTSSNMGVLVDWLVESLKYKLLPETLYLAISYVDRLYS 143

QY 114 SRRLPETNGWPLQVSVACLSLAKMEEPPLVPSLLDQIEGAKYIFEPRTIRRMELLVLG 173
DB 144 VNVL---NRQKLQLLVSSFLIASKYEETIKPKNVADF-VDITDNTYSQOEYVKMEADLLK 199

QY 174 VLDWRLRSYTPLCFLAF-ACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYW-----P 227
DB 200 TLKFEMGSPYKTFELGIRAVQENPDVPRKLF-----EFLANYLAELSLDDYGCLEFPV 253

QY 228 SCIAAAAILTANET-PN---WSVVKPENAESWCGLRKEKVIQCYQLMQEL 275
DB 254 SLIAASVTFLAFTIRPNVNPMSI-----ALQKCSGYKSKDKCECVLLHDL 300.

RESULT 12
CG2B_ORYSA STANDARD; PRT; 419 AA.
AC 040671;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycos2).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PIN GAEM 53;
RX MEDLINE=95261415; PubMed=7742859;
RA Sauter M., Mekhedov S.L., Kende H.;
RT "Gibberellin promotes histone H1 kinase activity and the expression
RT of cdc2 and cyclin genes during the induction of rapid growth in
RT deepwater rice internodes."
RL Plant J. 7:623-632(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. PIN GAEM 53;
RX STRAIN=CV. PIN GAEM 53;
RA Sauter M.;
RT "Isolation and characterization of a cDNA encoding a mitotic cyclin of
RT the CycB2 type from rice."
RL (In) Plant Gene Register PGR97-001.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
(MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X82036; CAA57556.1; -.
DR HSSP; P20248; IFTN.
DR InterPro: IPR000553; Cyclin.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 419 AA; 47572 MW; A8774B56BD839A5B CRC64;

Query Match 11.2%; Score 196.5; DB 1; Length 419;
Best Local Similarity 26.6%; Pred. No. 1.7e-10;
Matches 72; Conservative 43; Mismatches 123; Indels 33; Gaps 9;

QY 20 ILSGESPECSFSDIDSSPP-PSPTTEDCYSIASFIEHERNFVPGFEYLS-----RFQS 72
DB 128 VMGSELKEIEMEDIIEAAPDIDSCDANNSLAVEYVDEIYSFYRSEGISCVSPNYMSQ 187

QY 73 RSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPTNGWPLQVSVAC 132
DB 188 NDINEKMRGILIDWLEIVHYKLELDELTFLLVNIIDRFIARENVVRK---LQLVGTA 244

QY 133 LSLAKMEEPPLVPSLLDQIEGAKYIFEPRTIRRMELLVLGVLDWRLRSYTPLCFLAF- 191
DB 245 MLACKYEEVSVPYEDL-ILICDRAYTRTDILEMERKIVNTLQFDMSVPTPCFMRRL 303

QY 192 -ACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYWPSICIAAAAILTANETPNWSVKP 250
DB 304 KAAQSDKKLFLMSFF-----IIELSLVEYEMLKFPQPSMLAAAAIYTAQCTINGF----- 352

QY 251 ENAESW---CE---GLRKEKVIQCYQLMQEL 275

Db 353 ---KSNKCCCLHTKYSEQLMECSKMMVEL 380

RESULT 13

CG21_YEAST STANDARD; PRT; 471 AA.

AC P24868;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE G2/mitotic-specific cyclin 1.

GN CLB1 OR SCB1 OR YGR108W OR G5967.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91191554; PubMed=1849457;

RA Surana U., Robitsch H., Price C., Schuster T., Fitch I., Fletcher A.B.,

RA Nasmyth K.;

RT "The role of CDC28 and cyclins during mitosis in the budding yeast S.

RL cerevisiae.";

RL Cell 65:145-161(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91191555; PubMed=1849458;

RA Ghisla J.B., Richardson H.E., Sugimoto K., Henze M., Lew D.J.,

RA Wittenberg C., Reed S.I.;

RT "A cyclin B homolog in S. cerevisiae: chronic activation of the Cdc28

RT protein kinase by cyclin prevents exit from mitosis.";

RL Cell 65:163-174(1991).

RN [3]

RP SEQUENCE FROM N.A.

RA Wedler H., Scharfe M., Wedler E., Wambutt R.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M

CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 PROTEIN KINASE TO

CC FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE

CC ABRUPTLY DESTROYED AT MITOSIS.

CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED BEFORE MITOSIS. THE

CC LEVELS PEAK LATE IN THE G2 PHASE OF THE CELL CYCLE AND ARE AT A

CC MINIMUM IN G1 PHASE.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M65069; AAA34501.1; -

DR EMBL; M62389; AAA35019.1; -

DR EMBL; Z72893; CAA97112.1; -

DR PIR; A23700; A23700.

DR PIR; S14165; S14165.

DR HSSP; P30274; 1VIN.

DR SGD; S0003340; CLB1.

DR InterPro; IPR000553; Cyclin.

DR Pfam; PF00134; cyclin_1.

DR SMART; PF02984; cyclin_C; 1.

DR SMART; SM00385; CYCLIN; 2.

DR PROSITE; PS00292; CYCLINS; 1.

KW Cyclin; Cell cycle; Cell division; Mitosis; Multigene family.

SQ SEQUENCE 471 AA; 54870 MW; 4B347E96DD18735 CRC64;

Query Match 11.2%; Score 196.5; DB 1; Length 471;
Best Local Similarity 27.6%; Pred. No. 1.9e-10;
Matches 74; Conservative 42; Mismatches 111; Indels 41; Gaps 12;

OY 27 ECSFSDIDSPPPPTTEDCYSIASFIEHNEFVPGFEYLSRFQSRSLDANA----- 79

Db 189 EYEMDDDE-----EDC-DDPLMVSEEVNDI--FDYLHHLLEITLPPKANIYKHN 236

OY 80 ----REESVGMILKVHAYYGFQPLTAYLAVNYMDRLDSRRLPETNGWPLQVSVACLSL 135

Db 237 IKONNDILVNWIIKIHNFGLPETLYLAINIMDRFL-CEEVQLN--RLQVGTSCLEFI 293

OY 136 AAKMEPLVPSL--LDLQIEGAKYIFEPRTIRRMELLYGLVDMRLRSVTPLCFLAFAC 193

Db 294 ASKYEELXSPSIKHFAYETDACS--EDIKEGERFILEKLDFOISFANPMFLRIS- 349

OY 194 KVDSTGTFFIRFLISRATEIIVSNIQEASFAYWPSCIAAAILTANET--PNMSVVKPE 251

Db 350 KADYDIQSRTLAKFLMEI--SIVDFKFIGILPILCASAAFLSRKMLGKTWD---G 402

OY 252 NAESWCEGLRKEKVGICYOQLMDELVINN 279

Db 403 NLIHSGGYTKAKLYPVCQLMDYLVGS 430

OY 252 NAESWCEGLRKEKVGICYOQLMDELVINN 279

Db 403 NLIHSGGYTKAKLYPVCQLMDYLVGS 430

OY 252 NAESWCEGLRKEKVGICYOQLMDELVINN 279

Db 403 NLIHSGGYTKAKLYPVCQLMDYLVGS 430

RESULT 14

CGB2_HUMAN

ID CGB2_HUMAN STANDARD; PRT; 398 AA.

AC 095067;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE G2/mitotic-specific cyclin B2.

GN CCNB2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Kim D.G., Choi S.S., Kang Y.S., Lee K.H., Kim U.-J., Shin H.-S.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Saito T., Miyajima N.;

RT "G2/Mitotic-specific cyclin B2.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=21154917; PubMed=11230166;

RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,

RA Ansoerge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,

RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,

RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,

RA Wambutt R., Korn B., Klein M., Poustka A.;

RT "Towards a catalog of human genes and proteins: sequencing and

RT analysis of 500 novel complete protein coding human cDNAs.";

RL genome Res. 11:422-435(2001).

CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M

CC (MITOSIS) TRANSITION.

CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A

CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS

CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS

CC SUBSTRATE SPECIFICITY TO THE COMPLEX.

CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS

CC ABRUPTLY DESTROYED AT MITOSIS.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF002822; AAD09309.1; -

DR EMBL; AB020981; BAA78387.1; -.
DR EMBL; AL080146; CAB45739.1; -.
DR HSSP; P20248; 1J5U.
DR MIM; 602755; -.
DR InterPro; IPR00553; Cyclin.
DR Pfam; PF00134; cyclin_1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 2.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 398 AA; 45281 MW; 874466E1DD68A4C4 CRC64;

Query Match 11.1%; Score 196; DB 1; Length 398;
Best Local Similarity 26.5%; Pred. No. 1.7e-10;
Matches 83; Conservative 45; Mismatches 119; Indels 66; Gaps 13;

QY 12 LCGEDSSGILSGESPECSFSDIDS---SPPPSPTTEDCYSIASFIEHERNFVPGREYL 67
DB 105 LCQAFSDALL-----CKIEDIDNEDWENPQLCSDYKDIYQYLRQLEVLSINPHF--- 155
QY 68 SRFQSRSLDANAREESYGWILKVHAYYGFQPLTAYLVAVYMDRFLD---SRRLPETNGW 123
DB 156 --LDGRDINGRMRAILVDMVQVHSHKFRLLQETLYMCGIMDRFLQVQVSRK----- 206
QY 124 PLQLVSVACLSLAKMEEPVPSLLDLQIEGAKYI---FEPRTRRMELVVLGVLDWRL 179
DB 207 KIQLVGITALLLASKYEEMSPN-----IEDFVYITDNAYTSSQIREMETLILKELFEL 261
QY 180 RSVTPPLCFL--AFACKVD-STGTFIRFLISRATEIIVSNIOEASFLAYWPSCIAAAAIL 236
DB 262 GRPLPLHLRASKAGEVDEQHTLAKYLME-----LTLDYDMVHYHPSKVAALAAASC 314
QY 237 TRANET--PNMSVVKPENAESGCEGLRKEKVIQCYQLMOELVINNNOR----- 282
DB 315 LSQKVLGQGWNL-----KQYVYTYTENEVLEVMQHMKNVYKVENLTKETIAIKKYA 369
QY 283 --KLPLKVLPL 293
DB 370 SSKLKLKISMIPQL 382

RESULT 15

CG21_ANTMA STANDARD; PRT; 473 AA.
ID CG21_ANTMA

AC P34800;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin 1.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;

RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=94148008; PubMed=8313906;
RA Robert P.R.; Coen E.S.; Murphy G.J.P.; Doonan J.H.;

RT "Patterns of cell division revealed by transcriptional regulation of
RT genes during the cell cycle in plants."
RL EMBO J. 13:616-624(1994).

CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; X76122; CAA53728.1; -.
CC PIR; S41709; S41709.
CC HSSP; P30274; 1VIN.
CC InterPro; IPR00553; Cyclin.
CC Pfam; PF00134; cyclin_1.
CC Pfam; PF02984; cyclin_C; 1.
CC SMART; SM00385; CYCLIN; 2.
CC PROSITE; PS00292; CYCLINS; 1.
KW Cyclin; Cell cycle; Cell division; Mitosis.
SQ SEQUENCE 473 AA; 52704 MW; 502CF1735587638A CRC64;

Query Match 11.1%; Score 194.5; DB 1; Length 473;
Best Local Similarity 26.8%; Pred. No. 3e-10;
Matches 62; Conservative 44; Mismatches 104; Indels 21; Gaps 8;

QY 45 EDCYSIASFIEHERNFVPGFEYLSRFQSRSLDANAREESYGWILKVHAYYGFQPLTAYIA 104
DB 196 EDMYKFEYKSVENESR---PHDVMG--SQPEINEKMRALIDVWLVQVHKKFELSPETLYLT 250
QY 105 VNYMDRFLDSRRLPETNGWPLQLVSVACLSLAKMEEPVPSLLDLQIEGAKYIFEPRTI 164
DB 251 INIVDRYIASE---TTIRRELQVIGIGAMLIAASKYEETWAPVEVHEL-VCISDNTYSKQI 306
QY 165 RMELVVLGVLDWRLRSVTPPLCFAPACKVDSTGTFIRFLISRATEIIVSNIOEASFLA 224
DB 307 LVMEKRIIGALEWYLVTPPYVFLVRF-IKASMTDSDVENMYFLAELGMNY--ATLI 362
QY 225 YWPSCIAAAAILTA--ANEIPMSVVKPENAESWCEGLRKEKVIQCYQLM 272
DB 363 YCPSMIAAASVYAAARCTLNKAPFWNETIQLHT-----GFSEPQLMDCAKLL 408

Search completed: October 23, 2002, 14:38:29
Job time : 15 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:34:54 ; Search time 30 Seconds
(without alignments)
1954.843 Million cell updates/sec

Title: US-09-665-308D-12
Perfect score: 1758
Sequence: 1 MSVSCLSDYDLGEGDSSGIL.....SCKRRKLNRLNVDKGNSE 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPTREMBL_19:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organelle:*
- 10: sp_phage:*
- 11: sp_plant:*
- 12: sp_rodent:*
- 13: sp_virus:*
- 14: sp_vertebrate:*
- 15: sp_unclassified:*
- 16: sp_rv1rus:*
- 17: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	907.5	51.6	330	10 Q9SNV2	Q9snv2 antirrhinum
2	463.5	26.4	372	10 P93103	P93103 chenopodium
3	458.5	26.1	354	10 Q9ZRX9	Q9zrx9 nicotiana t
4	429.5	24.4	368	10 Q9SXM7	Q9sxn7 nicotiana t
5	425	24.2	373	10 Q9ZRX8	Q9zrx8 nicotiana t
6	423.5	24.1	343	10 Q9SNV1	Q9snv1 antirrhinum
7	420.5	23.9	308	10 Q9FKP7	Q9fkp7 arabidopsis
8	419.5	23.9	367	10 Q9FGQ7	Q9fgq7 arabidopsis
9	416.5	23.7	308	10 Q9XFR7	Q9xf7 arabidopsis
10	411	23.4	361	10 Q9SN11	Q9sn11 arabidopsis
11	403.5	23.0	336	10 Q9SMD4	Q9smd4 lycopersico
12	401	22.8	364	10 Q9SMD5	Q9smd5 lycopersico
13	383	21.8	359	10 Q9S7H9	Q9s7h9 lycopersico
14	370.5	21.1	384	10 Q82136	Q82136 pisum sativ
15	368	20.9	317	10 Q9LX96	Q9lx96 arabidopsis
16	367	20.9	386	10 Q40338	Q40338 medicago sa

17	364	20.7	378	10 Q9XG63	Q9xg63 medicago sa
18	355	20.2	367	10 Q9ZRX7	Q9zrx7 nicotiana t
19	354	20.1	361	10 Q9SNV0	Q9snv0 antirrhinum
20	351.5	20.0	349	10 Q82678	Q82678 chenopodium
21	340.5	19.4	302	10 Q9ZRX4	Q9zrx4 arabidopsis
22	322	18.3	222	10 Q9XG64	Q9xg64 medicago sa
23	276	15.7	321	10 Q9SZF6	Q9szf6 arabidopsis
24	247	14.1	454	10 Q9FVX0	Q9fvx0 arabidopsis
25	244	13.9	341	10 Q9LZM0	Q9lzm0 arabidopsis
26	228	13.0	502	10 Q43693	Q43693 ze mays (m
27	220	12.5	456	10 Q41732	Q41732 ze mays (m
28	218.5	12.4	482	10 Q40491	Q40491 nicotiana t
29	217.5	12.4	380	10 Q9AVT0	Q9avt0 picea abies
30	216.5	12.3	483	10 Q40514	Q40514 nicotiana t
31	216.5	12.3	483	10 Q40490	Q40490 nicotiana t
32	212.5	12.1	475	10 Q9XG14	Q9xg14 lycopersico
33	210.5	12.0	508	10 Q9SSZ6	Q9ssz6 oryza sativ
34	208.5	11.9	427	10 Q9CAX5	Q9cax5 arabidopsis
35	208.5	11.9	490	10 Q9XG15	Q9xg15 lycopersico
36	208	11.8	446	10 P93102	P93102 chenopodium
37	205	11.7	443	10 Q40794	Q40794 petroselinu
38	202.5	11.5	445	10 P93557	P93557 sesbania ro
39	201	11.4	425	10 Q39331	Q39331 brassica na
40	200.5	11.4	404	13 Q91BG1	Q91bg1 oryzias lat
41	200.5	11.4	452	10 Q49959	Q49959 lupinus lut
42	200	11.4	469	10 Q39878	Q39878 glycine max
43	199.5	11.3	401	13 Q9DGA4	Q9dga4 oryzias cur
44	199	11.3	398	11 Q922E9	Q922e9 mus musculu
45	199	11.3	437	10 Q9SBQ4	Q9sbq4 petunia hyb

ALIGNMENTS

RESULT 1

Q9SNV2 ID Q9SNV2 PRELIMINARY: PRT; 330 AA.
AC Q9SNV2: Q9SNV2: (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CYCLIN D1.
GN CYCD1.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaudin V., Lunness P., Robert P., Towers M., Riou-Khamlich C.,
RA Murray J., Coen E., Doonan J.H.;
RT "The expression of D-cyclin genes define distinct developmental zones
in Antirrhinum apical meristems and is locally regulated by the
RT cyclodea gene.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AJ250396; CAB61221.1; -
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SMO0385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 330 AA; 36494 MW; 7C7EF9C6382BBD2 CRC64;

Query Match 51.6%; Score 907.5; DB 10; Length 330;
Best Local Similarity 56.1%; Pred. No. 3.6e-83;
Matches 192; Conservative 52; Mismatches 77; Indels 21; Gaps 8;
QY 1 MSVSCLSDY-DLIGEDSSGILSG--ESPECSFSDIDSSPPPPPTTEDCYSTASFIH 56
||||| : |||||||||: || : || : ||::| |

Db 1 MSLSCSDCFSDLLCGEDSNIIIFSGGDDLPEYT-SDVESIP-----TDVDESIAGLLED 53
QY 57 ERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFOPLTAYLVNMDRFLDSRR 116
Db 54 ERD-LAGVN--SSSSNQSDSSTRTESTAWILKVQRYYGFOPLTAYLAVSYEDRFLNAHH 110
QY 117 LPETNGWPIQLVSVACLSLAAKMEEPVSLDLQIEGAKYIFEPRTIRRMELLVGLVD 176
Db 111 LPKLNGWPMQLLSVACLSLAAKMEESLVPSLLDQVEGANFIEEPRTIORMELLVRLVD 170
QY 177 WRLRSVTPLCFLAFACKVDSTGTFFIRFLISRATEIIVSNIOEASFLAWPSCIAAAAIL 236
Db 171 WRLRSISPFCTYLSFALKIDPTGYTGYFLTSRAKEIILSTVQETSLIEYRPSCIAAATML 230
QY 237 TAANEIPNWSVVPENAESWCEGLRKEKVGCYQLMQLVINNNQRLPLKVLPLQLRVT 296
Db 231 SSANDLPKFSFTAQHAEAWCDDLHKDNIASCLIKLIQGVESNNRPKKQP--KVLPLQLRVM 288
QY 297 TRTRMRSSTVSSFSSSSSTFSLSCKRRKLNRLWVDKGN 338
Db 289 TRASLASS-----ESSSSSTSSSPYKRRKLNNSRADDDKES 325

RESULT 2
P93103 PRELIMINARY; PRT; 372 AA.
AC P93103; 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CYCLIN-D LIKE PROTEIN.
GN CYCD1.
OS Chenopodium rubrum (Red goosefoot) (Pigweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
OX NCBI_TaxID=3560;
RN [1]
RP SEQUENCE FROM N.A.
RA Renz A., Fountain M., Beck E.;
RT "Nucleotide sequence of a cDNA encoding a D-type cyclin from a
RT photoautotrophic cell suspension culture of Chenopodium rubrum L.";
RL Plant Physiol. 0:0-0(0).
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; Y10162; CAA71244.1; -.
DR InterPro; IPR004366; Cyclin.
DR InterPro; IPR004367; Cyclin_C.
DR Pfam; PF00134; cyclin_1.
DR DR Pfam; PF02984; cyclin_1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 372 AA; 41768 MW; 6D5D1C91A5DB17CF CRC64;

Query Match 26.4%; Score 463.5; DB 10; Length 372;
Best Local Similarity 31.7%; Pred. No. 2.8e-38;
Matches 120; Conservative 66; Mismatches 116; Indels 77; Gaps 9;

QY 9 YDLICGEDSSGILSGESPECSFSDIDSSPPPTEDCYSI----- 50
Db 5 FDLICAEEDNSSI-----FDEYVDN--YGVVDDVLIQICNLQOQHGNLRNFDEFTL 53
QY 51 -----ASFIEHERNFVPGFEYLSRFQSRSLDANAREESV 84
Db 54 ILLIIEKHENEALLISGFVANHECLASLFEDNERQHFLGLDYLKRFNGDDLGAARNLVI 113
QY 85 GWILKVHAYYGFOPLTAYLVNMDRFLDSRRLPETNGWPIQLVSVACLSLAAKMEEPV 144
Db 114 DWIHKVQSHYNGPLCYLSVNYLDRFLSAVELP-GKAMMMQLLGVACLSLAAKVDETDV 172
QY 145 PSLDLQIEGAKYIFEPRTIRRMELLVGLVDWRLRSVTPLCFLAFACKVDSTGTFFIR 204
Db 173 PLILDLQVSESKVFEAKTIQRMELLVSLTKWRMQSVTPPSFIDYFLYKLSGDKMPSKS 232

QY 205 LISRATEIIVSNIOEASFLAYWPSCIAAAAILTAANEIPNWSVK-PENAESW-CEGLRK 262
Db 233 LIFQAIQLILSTIKGIDLMERFSEIAAAVAISVTQQT---QIVEFTDKAFSFLTDHVEK 289
QY 263 EKVIQCYQLMQLVINNNQRLPLKVLPLQLRVTTRTRMRSSTVSSFSSSSSTFSLSC- 321
Db 290 ERLMKCVEIMHDLRMSRSNGALASTSVQSPGLVLD--ASACLSYKSDDTSTPSSGSCG 347
QY 322 -----KRRKLN 327
Db 348 NSAHSSPASAPPPKRRKLD 366

RESULT 3
Q9ZRX9 PRELIMINARY; PRT; 354 AA.
AC Q9ZRX9; 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CYCLIN D2.1 PROTEIN.
GN CYCD2.1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99097070; PubMed=9880377;
RA Sorrell D.A., Combettes B., Chaubet-Gigot N., Gigot C., Murray J.A.H.;
RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels
RT of Transcripts in Tobacco Bright Yellow-2 Cells";
RL Plant Physiol. 119:343-351(1999).
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ011892; CAA09852.1; -.
DR InterPro; IPR004366; Cyclin.
DR InterPro; IPR004367; Cyclin_C.
DR Pfam; PF00134; cyclin_1.
DR DR Pfam; PF02984; cyclin_1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 354 AA; 39714 MW; 18363A0E786E89BF CRC64;

Query Match 26.1%; Score 458.5; DB 10; Length 354;
Best Local Similarity 36.0%; Pred. No. 8.4e-38;
Matches 120; Conservative 63; Mismatches 127; Indels 23; Gaps 9;

QY 5 CLSDYDILCGEDSSGILSGESPECSFSD-IDSSPPPSPT-TEDCYSIASFIEHERNFV 62
Db 23 CFDDVDVSLTISQON--IETKSKDLSFNNGIRSEPLIDLPSLSECSISF--MVOREMEFLP 78
QY 63 GFEYLSRFQSRSLDANAREESVGWILKVHAYYGFOPLTAYLVNMDRFLDSRRLPETNG 122
Db 79 KDDYVERLRSGDDLDSVRKEALDWILKAHMYGFGLSFCLSINYLDRLSLYELPRSKT 138
QY 123 WPIQLVSVACLSLAAKMEEPVSLDLQIEGAKYIFEPRTIRRMELLVGLDWRLRSV 182
Db 139 WTVQLAVACLSLAAKMEEINVPPLTVDLQVGDPKFVEGKTIQRMELLVSLTKWRMQAY 198
QY 183 TPCLFLAFACKVDSTGTFFIRFLISRATEIIVSNIOEASFLAYWPSCIAAAAILTAANEI 242
Db 199 TPYTFIDYFMKRMNGDQIPSRPLISGSMQLLSIIRSIDFLERSSSEIAASVAMSVEI 258
QY 243 PNWSVVKPENAESWCEGLRKEKVGICYQLMQLVINNNQRLPLKVLPLQLRVT-----LRVT 297
Db 259 QAKDIDKA--MPCFIIHLDKGRVQKVELIQLDT-TATITTTAAASLVPQSPIGVLEAAA 315
QY 298 RTRMRSS--TVSSFSSSSSTFSLSCKRRKLN 327
Db 316 CLSYKSGDERTVSGCTTSSHT-----KRRKLD 342

RESULT 4

Q9SXN7 PRELIMINARY; PRT; 368 AA.

AC Q9SXN7; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE MTCYCD3-1 PROTEIN.

GN MTCYCD3-1.

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4097;

RN [1]

RP SEQUENCE FROM N.A.

RA Sekine M.;

RT "Cell cycle regulated gene.";

RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR EMBL: AB015222; BAA76478.1; -.

DR InterPro: IPR004366; Cyclin.

DR InterPro: IPR004367; Cyclin_C.

DR Pfam: PF00134; cyclin_1.

DR Pfam: PF02984; cyclin_C; 1.

DR SMART: SM00385; CYCLIN; 1.

DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.

KW Cell cycle; Cell division; Cyclin.

SW SEQUENCE 368 AA; 42827 MW; CDF280F18360180B CRC64;

Query Match 24.4%; Score 429.5; DB 10; Length 368;

Best Local Similarity 34.7%; Pred. No. 7.5e-35;

Matches 104; Conservative 56; Mismatches 123; Indels 17; Gaps 4;

OY 24 ESPECSFSDIDSSPPSPPTTE-DCY----STASFIEHERNFVPGFEYLSRFQSRSLDAN 78

Db 30 ETIEDEILEKEATLPPLPLEQDLFWEDDELISLFTKEKETISNEET--KTDPLCL 86

OY 79 AREESVGWILKVHAYYGFQPLTAYLVNVMDFLDSRLPETNGWPLQLVSVACLSLAAK 138

Db 87 SRKEAVKWLKVNAHYGFSTFTAILAINYFDRFLSLHFQKDKPMWIDLVAVTCLSLAAK 146

OY 139 MEPLVPSLDLQIEGAKYIFEPRTIRRMELVLGVLDWRLRSVTPPLCLAFACKVDST 198

Db 147 VEETQVPLLDQVEDAKYVEAKTIQRMELVLSLKRMPNPTPLSEFVHIIIRIGLK 206

OY 199 GTFIRFLISRATETIVSNIQEASFLAYWPSCIAAAIITLANEIPNWSVVM PENAESWCE 258

Db 207 SHIWEFLKQECERILLVLADCRFLSYMPSVATATMLHVIHOVEPCNADLYQNQLLEVL 266

OY 259 GLRKEKVIQCYQLMOELVINNNQRLPLKVLPLQLRVTTTRTMRSSVSSSSSSSTFS 318

Db 267 NISKEKVNDCYELITEVSNSISHK-----RKYESPINSPSAVIDFHYSSSENSNES 317

RESULT 5

Q9ZRX8 PRELIMINARY; PRT; 373 AA.

AC Q9ZRX8; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CYCLIN D3.1 PROTEIN.

GN CYCD3.1.

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

OX NCBI_TaxID=4097;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99097070; PubMed=9880377;

RA Sorrell D.A., Combettes B., Chaubet-Gigot N., Gigot C., Murray J.A.H.;

RT "Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels

RT of Transcripts in Tobacco Bright Yellow-2 Cells.";

RL Plant Physiol. 119:343-351(1999).

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR EMBL: AJ011893; CAA09853.1; -.

DR InterPro: IPR004366; Cyclin.

DR InterPro: IPR004367; Cyclin_C.

DR InterPro: IPR002114; Pts_Hpr_ser.

DR Pfam: PF00134; cyclin; 1.

DR Pfam: PF02984; cyclin_C; 1.

DR SMART: SM00385; CYCLIN; 1.

DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.

DR PROSITE: PS00589; Pts_Hpr_ser; UNKNOWN_1.

KW Cell cycle; Cell division; Cyclin.

SW SEQUENCE 373 AA; 42980 MW; 597F0994EDBCD4D4 CRC64;

Query Match 24.2%; Score 425; DB 10; Length 373;

Best Local Similarity 42.9%; Pred. No. 2.2e-34;

Matches 90; Conservative 36; Mismatches 84; Indels 0; Gaps 0;

OY 66 YLSRFGSRSLDANAREESVGWILKVHAYYGFQPLTAYLVNVMDFLDSRLPETNGWPL 125

Db 89 WFNSEQDSSLCSARVDSVEWILKNGYGFSALEAVLAIFYDRFLTSLHYQDKPMMI 148

OY 126 QLVSVACLSLAAKMEPLVPSLDLQIEGAKYIFEPRTIRRMELVLGVLDWRLRSVTP 185

Db 149 QLAVYCLSLAAKVEETQVPLLDQVEDAKYVEAKTIQRMELVLSLKRMPNPTPL 208

OY 186 CFLAFACKVDSTGTGTFIRFLISRATETIVSNIQEASFLAYWPSCIAAAIITLANEIPNW 245

Db 209 SFLDHITRLGLRNINHWELRRCENLLSIMADCRVRYMPSVATATMLHVIHOVEPC 268

OY 246 SVKPENAESWCEGLRKEKVIQCYQLMOEL 275

Db 269 NSVDYQNQLLVGLKINKKVNCFELISEV 298

RESULT 6

Q9SNV1 PRELIMINARY; PRT; 343 AA.

AC Q9SNV1; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CYCLIN D3A (FRAGMENT).

GN CYCD3A.

OS Antirrhinum majus (Garden snapdragon).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.

OX NCBI_TaxID=4151;

RN [1]

RP SEQUENCE FROM N.A.

RA Gaudin V., Lunness P., Robert P., Towers M., Riou-Khamlichl C.,

RA Murray J., Coen E., Doonan J.H.;

RT "The expression of D-cyclin genes define distinct developmental zones

RT in Antirrhinum apical meristems and is locally regulated by the

RT cycloidea gene.";

RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.

DR EMBL: AJ250397; CAB61222.1; -.

DR InterPro: IPR004366; Cyclin.

DR InterPro: IPR004367; Cyclin_C.

DR Pfam: PF00134; cyclin; 1.

DR Pfam: PF02984; cyclin_C; 1.

DR SMART: SM00385; CYCLIN; 1.

DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.

KW Cell cycle; Cell division; Cyclin.

FT NON_TER 343

SW SEQUENCE 343 AA; 39254 MW; 128210AB2FC6E2C6 CRC64;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RA de Veylder L., De Almeida Engler J., Bursens S., Manevski A.,
RA Lescure B., Van Montagu M., Engler G., Inze D.;
RT "A new D-type cyclin of Arabidopsis thaliana expressed during lateral
RT root primordia formation."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AJ131636; CAB41347.1; -
DR InterPro; IPR004367; Cyclin_C.
DR InterPro; IPR004367; Cyclin_C.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 308 AA; 34687 MW; 591ADA3361DD63D CRC64;

Query Match 23.7%; Score 416.5; DB 10; Length 308;
Best Local Similarity 34.6%; Pred. No. 1.2e-33;
Matches 100; Conservative 52; Mismatches 96; Indels 41; Gaps 7;

OY 8 DYDLGCE--DSSGILSGES-----PECSFSDIDSSPPSPPTTEDCYSIASFIEHER 58
DB 7 ELSTICTESNVDECMIVDETPETISIFQMGFSQSESE-----TIMEMVEKEK 55
OY 59 NFVPGFEYLSRFQSRSLDAN-AREESVGWILKVHAYYGQPLTAYLVNMDRFLDSRRL 117
DB 56 QHLPSPDYIKRLRSGLDLNVGRDALNMIWKACEVHGFPLCFCLAMNLDRLSVHDL 115
OY 118 PETNGWPLQVSVACLSLAKMEEPVPSLLDQIEGAKYIFEPRTIRRMELVLTGLVDW 177
DB 116 PSGKWIQLQVLAACLSLAKIEETVPMILDLQVGPQFVFEAKSVQRMELVLTGLVDW 175
OY 178 RLRSVTPICLAF-----ACKVDSITGTFIRFLISRATEIIVSNIOEASFLAYWPCIAA 232
DB 176 RLRAITPCSTIRYFLRKMSKCDQEPSNT-----LISRSLQVIASITTKGIDLEFRPSEAA 231
OY 233 AAILTAANEI-----PNMSVVKPENAESWCGLRKEKVIQCYQ 270
DB 232 AVALSVSGELQVRVHFDNSSFSPLFLQKRVKKIGEMIESDGSDLCSQ 280

RESULT 10

O9SN11

ID O9SN11 PRELIMINARY; PRT; 361 AA.

AC O9SN11;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE CYCLIN D3-LIKE PROTEIN (AT3G50070/F3A4_150).

GN F3A4.150.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Barques M., Collado M.C., Navarro P., Terol J., Perez-Alonso M.,

RA Mewes H.W., Lemcke K., Mayer K.F.X., Quettler F., Salanoubat M.;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Natusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Becker J.R.;

RT "Arabidopsis cDNA clones."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL; AL132978; CAB62115.1; -
DR EMBL; AY052665; AAK96569.1; -
DR InterPro; IPR004366; Cyclin.
DR InterPro; IPR004367; Cyclin_C.
DR InterPro; IPR003880; Phosphopant_attach.
DR Pfam; PF00134; cyclin; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 361 AA; 41737 MW; DBBE9329A33B9D02 CRC64;

Query Match 23.4%; Score 411; DB 10; Length 361;
Best Local Similarity 31.4%; Pred. No. 5.4e-33;
Matches 109; Conservative 59; Mismatches 119; Indels 60; Gaps 7;

OY 6 LSDYDLGCE--DSSGILSGESPECSFSDIDSSPPSPPTTEDCYSIASFIEHERNFVPGFE 65
DB 49 LSDHDLMDDELSTLISKQEPCLYDEI-----LDD-----E 80
OY 66 YLSRFQSRSLDANAREESVGWILKVHAYYGQPLTAYLVNMDRFLDSRRLPETNGWPL 125
DB 81 FL-----VLCKEALDWIFKVKSHYGFNSLTALLAVNYEDRITSRKQOTDKPMMS 131
OY 126 QVSVACLSLAKMEEPVPSLLDQIEGAKYIFEPRTIRRMELVLTGLVDWRLRSVTPPL 185
DB 132 QVTLACLSLAKMEEPVPSLLDQIEGAKYIFEPRTIRRMELVLTGLVDWRLRSVTPPI 191
OY 186 CFLAFACKVDSTGTFIRFLISRATEIIVSNIOEASFLAYWPCIAAAILTAANEIPNW 245
DB 192 SEFDHIIIRYSFKSHQLEFLSRCESLSTIPDSRFLSFSPLATVAINVSVIRDLKMC 251
OY 246 SVKPENAESWCGLRKEKVIQCYQLMQLVINNQRKPLKLVLPQ----LRVTRTRM 301
DB 252 DEAVYQSQLMTLTKVDSEKVNKC-----ELVLDHSPSKRRMMNMQOPASPIGVFASFS 307
OY 302 RSSTVSSFSSSSSTFSLS-----CKRRKLN-----NRLWVD 333
DB 308 SDDSNSWVVSASAVSSPSSEPLKRRRVQEQOMRLSSINRMFFD 354

RESULT 11

O9SMD4

ID O9SMD4 PRELIMINARY; PRT; 336 AA.

AC O9SMD4;

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE CYCD3.3 PROTEIN.

GN CYCD3.3.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI_TaxID=4081;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. UC82B;

RX MEDLINE=20566012; PubMed=11113158;

RA Kvarneden A., Yao J.L., Zhan X., O'Brien I., Morris B.;

RT "Isolation of three distinct CycD3 genes expressed during fruit
RT development in tomato.";

RL J. Exp. Bot. 51:1789-1797(2000).


```
Db 127 FQKPKFMSQLAAVACLSIAKVEETQVPLLDLOYADSRFVFEAKTIQRMELLVSTLK 186
QY 177 WRLRSVTPCLFLAFACKVDSTGTFRFLISRATEIIVSNIOEASFLAYWPCIAAAAIL 236
Db 187 WKMLVTPLSFIDHIMRRFGFMSNLHMDFLKCKERLIDITDSRLHYPPSVIATASMF 246
QY 237 TAANEIPNWSVVKPENAESW-----CEGLRKEKY-IGCYQIMQELVIN 278
Db 247 YVINDI-----EPSNAMEYQNLMSVLKVRKDIFFECHDLILEMDTACYKLCQSL--- 297
QY 279 NNQRKLPCLKVLPLQRTVTRFRMRSTVS-SFSSSSSTSFSLCKRKLNNR 329
Db 298 --KRKHRSVPGSPSGVIDAYFSSESSNESMSVASSISSPEPQYKRKNTQDQ 347
```

```
RESULT 14
082136 PRELIMINARY; PRT; 384 AA.
AC 082136;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CYCLIN D.
GN CYCD1.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98249622; PubMed=9588023;
RA Shimizu S., Mori H.;
RT "Analysis of cycles of dormancy and growth in pea axillary buds based
RT on mRNA accumulation patterns of cell cycle-related genes.";
RL Plant Cell Physiol. 39:255-262(1998).
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AB008188; BAA33153.1; -.
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 384 AA; 43859 MW; 34BC092B3C72E359 CRC64;
```

Query Match 21.1%; Score 370.5; DB 10; Length 384;
Best Local Similarity 35.3%; Pred. No. 7.2e-29;
Matches 94; Conservative 42; Mismatches 83; Indels 47; Gaps 7;

```
QY 80 REESVGMILKVHAYYGFQPLTAVLVNMDRFLDSRLPETNGWPLQLVSVACLSIAKM 139
Db 105 RREAQVMMLKVNAHYAFSPLTATLVYFDRFLTFHQDKRPMIQLVAVTCISIAKY 164
QY 140 EEPVPSLLDLQIEGAKYIFEPRTIRRMELLVGLVDMRLRSVTPCLFLAFACKVD-ST 198
Db 165 EETQVPLLDLQVQDTKYVFEAKTIQRMELLILSTLKKMHPVTPHSFLDHIITRLGKT 224
QY 199 GTFIRFLISRATEIIVSNIOEASFLAYWPCIAAAAILTAANEIPN-----WS 246
Db 225 NLHWEFL-RRCENLLSVLLDSRVGCVPSVLATATMLHVIDQIEESDNGVDYKQLLS 283
QY 247 VVKPENAESWCEGLRKEKYIGCYQIMQELVINNN--QRKLPCLKVLPLQLRTVTRMRS 303
Db 284 ILK-----INKEKVDECYNAIVEVTNENNYGHRKRYEQIIPGSP-----S 322
QY 304 STVSSFSSS-----SSTSFSL 320
Db 323 GVIDAVFSSDGSNDMSWKVGSSSYSTS 348
```

```
RESULT 15
Q9LX96 PRELIMINARY; PRT; 317 AA.
ID Q9LX96
AC Q9LX96;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CYCLIN PROTEIN-LIKE.
GN F12B17_210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL353995; CAB89399.1; -.
DR InterPro: IPR004366; Cyclin.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
SQ SEQUENCE 317 AA; 35910 MW; 07616F8480927711 CRC64;
```

Query Match 20.9%; Score 368; DB 10; Length 317;
Best Local Similarity 35.5%; Pred. No. 9.9e-29;
Matches 104; Conservative 47; Mismatches 104; Indels 38; Gaps 8;

```
QY 50 IASFIHERNVPGFEYLSRFQSRSLDANAREESVGMILKVHAYYGFQPLTAVLVNMD 109
Db 39 VREMIEKERQHSPPDDYLKRLRNGDLDFNVRIQALGWIKACELOFGPLCICLAMNYLD 98
QY 110 RFLDSRRLPETNGWPLQLVSVACLSIAKMEEPVPSLLDLQIEGAKYIFEPRTIRMEL 169
Db 99 RFLSVHDLPSGRAWTVQLAVACLSIAKIEETNPPELMQLQYGAPMVFVFAKSVQRMEL 158
QY 170 LVLGVLDMRLSVTPCLFLAFACKVDSTGTFRF-LISRATEIIVSNIQ----- 218
Db 159 LVLNVLRLRRAVTPCSYVRFLSKINGYDQEPHSRLVTRSLQVIASTTKGDRGLGFEFK 218
QY 219 -----EASFLAYWPCIAAAAILTAANE-IPNWSVVKPENAESWCEGLRKEKY--I 266
Db 219 GVLIVDVWAGIDFLFRASEIAAAVALSVSGEHFDKFSF-----SSFSLEKEERYKI 272
QY 267 GCYQLMQELVINNNQRKLPCLKVLPLQRTVTRTRMRSSTVSSFS-SSSSTFS 318
Db 273 G---EMIERDSSSSSQTPNNTYV-----QFKSRRYSHSLSTASVSSSLTSL 317
```

Search completed: October 23, 2002, 14:39:07
Job time : 32 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:37:34 ; Search time 13 Seconds
(without alignments)
636.944 Million cell updates/sec

Title: US-09-665-308D-12
Perfect score: 1758
Sequence: 1 MSVSCLSPYDLGCGEDSSGI.....SCKRRKLNRLWDDKGNSE 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.5	10.3	432	1	US-08-522-166-8 Sequence 8, Appl1
2	180.5	10.3	432	1	US-08-488-382A-8 Sequence 8, Appl1
3	180.5	10.3	432	2	US-08-480-912-8 Sequence 8, Appl1
4	177.5	10.1	295	2	US-08-464-517-19 Sequence 19, Appl1
5	177.5	10.1	295	2	US-08-246-361A-19 Sequence 19, Appl1
6	177.5	10.1	295	3	US-08-463-772-19 Sequence 19, Appl1
7	177.5	10.1	295	5	PCT-US93-05000-2 Sequence 2, Appl1
8	177.5	10.1	295	5	PCT-US93-05000-19 Sequence 19, Appl1
9	177.5	10.1	309	2	US-08-464-517-4 Sequence 4, Appl1
10	177.5	10.1	309	3	US-08-463-772-4 Sequence 4, Appl1
11	176.5	10.0	289	2	US-08-246-361A-4 Sequence 4, Appl1
12	176.5	10.0	289	5	PCT-US93-05000-4 Sequence 4, Appl1
13	173.5	9.9	662	2	US-08-770-761A-5 Sequence 5, Appl1
14	173.5	9.9	705	2	US-08-770-761A-7 Sequence 7, Appl1
15	171.5	9.8	295	1	US-07-947-120-8 Sequence 8, Appl1
16	171.5	9.8	295	1	US-08-472-893A-8 Sequence 8, Appl1
17	171.5	9.8	295	2	US-08-460-694-2 Sequence 2, Appl1
18	171.5	9.8	295	3	US-08-460-744-2 Sequence 2, Appl1
19	171.5	9.8	295	3	US-07-667-711B-2 Sequence 2, Appl1
20	171.5	9.8	295	3	US-08-947-492-8 Sequence 8, Appl1
21	171.5	9.8	618	2	US-08-770-761A-3 Sequence 8, Appl1
22	171.5	9.8	647	2	US-08-770-761A-8 Sequence 8, Appl1
23	171.5	9.8	660	2	US-08-770-761A-2 Sequence 2, Appl1
24	171	9.7	150	2	US-08-460-694-3 Sequence 3, Appl1
25	171	9.7	150	3	US-08-460-744-3 Sequence 3, Appl1
26	171	9.7	150	3	US-07-667-711B-3 Sequence 3, Appl1
27	170	9.7	236	2	US-08-464-517-22 Sequence 22, Appl1

28	170	9.7	236	2	US-08-246-361A-22	Sequence 22, Appl1
29	170	9.7	236	3	US-08-463-772-22	Sequence 22, Appl1
30	170	9.7	236	5	PCT-US93-05000-22	Sequence 22, Appl1
31	169.5	9.6	295	2	US-08-464-517-2	Sequence 2, Appl1
32	169.5	9.6	295	2	US-08-246-361A-2	Sequence 2, Appl1
33	169.5	9.6	295	3	US-08-463-772-2	Sequence 2, Appl1
34	167.5	9.5	295	2	US-08-464-517-20	Sequence 20, Appl1
35	167.5	9.5	295	2	US-08-246-361A-20	Sequence 20, Appl1
36	167.5	9.5	295	3	US-08-463-772-20	Sequence 20, Appl1
37	167.5	9.5	295	5	PCT-US93-05000-20	Sequence 20, Appl1
38	167	9.5	292	2	US-08-464-517-23	Sequence 23, Appl1
39	167	9.5	292	2	US-08-246-361A-6	Sequence 6, Appl1
40	167	9.5	292	2	US-08-246-361A-23	Sequence 23, Appl1
41	167	9.5	292	3	US-08-463-772-23	Sequence 23, Appl1
42	167	9.5	292	5	PCT-US93-05000-23	Sequence 23, Appl1
43	165	9.4	492	1	US-08-463-090B-10	Sequence 10, Appl1
44	162.5	9.2	291	5	PCT-US93-05000-6	Sequence 6, Appl1
45	160	9.1	404	2	US-09-092-770-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-522-166-8
; Sequence 8, Application US/08522166
; Patent No. 5783661
; GENERAL INFORMATION:
; APPLICANT: Roberts, J.M.; Ohtsubo, M; Koff, A.C.; Cross, F.
; TITLE OF INVENTION: Human Cyclin E
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
; COMPUTER: IBM PC Compatible/Pentium
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,166
; FILING DATE: June 7, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,309
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHRO-1-8597
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; US-08-522-166-8
Query Match 10.3%; Score 180.5; DB 1; Length 432;
Best Local Similarity 29.3%; Pred. No. 3.3e-12;
Matches 75; Conservative 31; Mismatches 101; Indels 49; Gaps 10;

QY 16 DSSGILSGESPECSFSDIDSSPPPTTEDCYSIASFIEHERNFVPGFEYLSRFSQSRSL 75
159 DMSIVLEDEKP-----VSVNENP-----DYHEDIHTYLR--EMEYKCKPKVGYMKK--QPD1 206
QY 76 DANAREESVGMILKVHAYYGFQPLTAYLVNMYDRFLDSRRLEPBTNGWPLQVSVACISL 135
207 TNSMRALVDMVLEVEGEEYKIQNETLHLAVNYIDRFLSSMSVLRGK--LQVGTAAAML 263
QY 136 AAKMEELVPSLIDLIQIEGAKYI---FEPTIRRMELLYGLVDMRLRSVTPLCFLAF 191
264 ASKFEELYPPEVAEF-----YITDDTYTKKQVLRMEHLVKVLTFDLAAPTVNQFLQY 318
QY 192 -----ACKVDSTGTFFIRFLISRATIELIVSNIOEASFLAYWPSICIAAAAILTAANEIPN 244
319 FLHQOPANCKVESLAFMLGEL-----SLIDADPYLKLYPSVIAGAAPHALTYTV-- 367
Db 245 MSVVKPENAESWCEGL 260
QY 368 -----TGQSWPEST 376

RESULT 2

US-08-488-382A-8
; Sequence 8, Application US/08488382A
; Patent No. 5807698
; GENERAL INFORMATION:
; APPLICANT: Roberts, J.M.; Ohtsubo, M.; Koff, A.C.; Cross, F.
; TITLE OF INVENTION: Human Cyclin E
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,382A
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,309
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHRO-1-8600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; US-08-488-382A-8

Query Match 10.3%; Score 180.5; DB 1; Length 432;
Best Local Similarity 29.3%; Pred. No. 3.3e-12;
Matches 75; Conservative 31; Mismatches 101; Indels 49; Gaps 10;
QY 16 DSSGILSGESPECSFSDIDSSPPPTTEDCYSIASFIEHERNFVPGFEYLSRFSQSRSL 75
159 DMSIVLEDEKP-----VSVNENP-----DYHEDIHTYLR--EMEYKCKPKVGYMKK--QPD1 206

Db 159 DMSIVLEDEKP-----VSVNENP-----DYHEDIHTYLR--EMEYKCKPKVGYMKK--QPD1 206
QY 76 DANAREESVGMILKVHAYYGFQPLTAYLVNMYDRFLDSRRLEPBTNGWPLQVSVACISL 135
207 TNSMRALVDMVLEVEGEEYKIQNETLHLAVNYIDRFLSSMSVLRGK--LQVGTAAAML 263
QY 136 AAKMEELVPSLIDLIQIEGAKYI---FEPTIRRMELLYGLVDMRLRSVTPLCFLAF 191
264 ASKFEELYPPEVAEF-----YITDDTYTKKQVLRMEHLVKVLTFDLAAPTVNQFLQY 318
QY 192 -----ACKVDSTGTFFIRFLISRATIELIVSNIOEASFLAYWPSICIAAAAILTAANEIPN 244
319 FLHQOPANCKVESLAFMLGEL-----SLIDADPYLKLYPSVIAGAAPHALTYTV-- 367
Db 245 MSVVKPENAESWCEGL 260
QY 368 -----TGQSWPEST 376

RESULT 3

US-08-480-912-8
; Sequence 8, Application US/08480912
; Patent No. 5861259
; GENERAL INFORMATION:
; APPLICANT: Roberts, J.M.; Ohtsubo, M.; Koff, A.C.; Cross, F.
; TITLE OF INVENTION: Immunoassays for Detection of Human Cyclin E
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
; OPERATING SYSTEM: MS-Windows 3.1
; SOFTWARE: Word for Windows-6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,912
; FILING DATE: June 7, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,309
; FILING DATE: September 20, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHRO-1-8599
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
; TELEFAX: 1-206-224-0779
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; US-08-480-912-8

Query Match 10.3%; Score 180.5; DB 2; Length 432;
Best Local Similarity 29.3%; Pred. No. 3.3e-12;
Matches 75; Conservative 31; Mismatches 101; Indels 49; Gaps 10;
QY 16 DSSGILSGESPECSFSDIDSSPPPTTEDCYSIASFIEHERNFVPGFEYLSRFSQSRSL 75
159 DMSIVLEDEKP-----VSVNENP-----DYHEDIHTYLR--EMEYKCKPKVGYMKK--QPD1 206

```

QY      76  DANAREESVGMI LKVHAYYGEOPLTAVLAVNYMDRFLDSRRLPETNGWPIQLVSVACLSL 135
      : | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     207  TNSMRAILVDWLVEVGEEYKIQNETHLAVNYIDRFLSSMSVLRGK--LQLVGTAMLL 263
      : | : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     136  AAKMEEPVPSL LDIQIEGAKYI---FEPTIRRMELLVGLDWRLRSTVPLCFIAF 191
      | : | | : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     264  ASKEEIEYPRVEAEF-----VYITDDTYTKQVLRMEHLVLYKVLTFDLAAPTIVNQFLTYQ 318
      : | : | : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     192  -----ACKVDSTGT FIRFLISRATETIVSNIQEASF LAYWPSCIAAAILTAANEIPN 244
      : | : | : | : : : : : : : : : : : : : : : : : : : : : : :
Db     319  FLHQQPANCKVESIAMFLGEL-----SLIDADPYLKYLP SVIAGAFHLALYTV-- 367
      : | : | : | : : : : : : : : : : : : : : : : : : : : : : :
QY     245  WSVVKPENAESWC EGL 260
      : | : | : |
Db     368  -----TGQSWPEST 376

```

```

: RESULT 4
: US-08-464-517-19
: Sequence 19, Application US/08464517
: Patent No. 5869640
: GENERAL INFORMATION:
: APPLICANT: BEACH, David H.
: TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
: NUMBER OF SEQUENCES: 50
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII(text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,517
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/963,308
: FILING DATE: 16-OCT-1992
: APPLICATION NUMBER: US 07/888,178
: FILING DATE: 26-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,514
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Matthew P. Vincent
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MI-004C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 295 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-464-517-19

```

Query Match	10.1%;	Score 177.5;	DB 2;	Length 295;
Best Local Similarity	25.28;	Pred. No. 4e-12;		
Matches 56;	Conservative 45;	Mismatches 108;	Indels 13;	Gaps 6;

OY 50 IASFIHERNFVPGFEFYLRSRQSSNLDANAREESVGWILKVHAYYGQPLTAVLAVNYMD 109
 :: :: | | | : : : : : : :
Db 28 LRAMLKAEETCAPSVSYFKCYQKEVL-PSMRKIIVATWMLEVCCEOKCEEYVPDIAMNYLD 86

```

QY 110 RFDSRRLPETNGWPLQOLVSACLSIAAKMEE--PLVPSLLDLOIEGAKYIIEPRTIRM 167
    ||| : : : ||| : : : ||| | | : : : |
Db 87 RFLSLEPVKKSR--LQLLGATCMFVASKMKETIPLTAEKLCITYTDS--IRPELLQM 140
    ||| : | | : : ||| : | : : : |
QY 168 ELLVGLVDWRLRSVTPLCFLAFACKVDSTGTGFI RFLISRATEIIVSNIQEASFLAYWP 227
    ||| : | | | : : ||| : | : : : |
Db 141 ELLLVNKLKWNLAAMTPHDFIEHFLSKMPEAEENKQIIRKHAQTVALCATDYKFISNPP 200
    ||| : | | | : : ||| : | : : : |
QY 228 SCIAAAAILTAANEIIPNMSVVKPENAESWCGLR-KEKYIGC 268
    | : || : : | : : : | | : : ||| |
Db 201 SMVAAGSVVAA---VKGLNLRSPNNFLSYRLTRFLSRVIKC 239

```

```

RESULT 5
US-08-246-361A-19
; Sequence 19, Application US/08246361A
; Patent No. 5998582
;
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIT-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-246-361A-19

```

Query Match	10.1%;	Score 177.5;	DB 2;	Length 295;
Best Local Similarity	25.2%;	Pred. No. 4e-12;		
Matches	56;	Conservative	45;	Mismatches 108;
				Indels 13;
				Gaps 6;

OY	50	IASEIEHERNNFVPGFEYLSRFQSSSLDANAREESVGWLKVAHYGQPLTAYLAVNYMD	109
		: : : : : : : : : : : : : :	
Db	28	LRAMLAEEETCAPSVSYFKCVQKEVL-PSMRKIYATVMTLECCGEOKCEEEFEPYLANYYID	A6

```
QY 110 RFLDSRRRLPETNGWPLQLOYSVACISLAKMEE--PLVPSLDLQIEGAKYIFEPRTIRRM 167
    ||| : :: ||| : : : ||| : || : : : ||
Db 87 RFLSLPEVKKSR---LQLLGATCMFVASKMKETIPLTAEKICITYDGS---IRPEELQOM 140
```


TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-19

Query Match 10.1%; Score 177.5; DB 5; Length 295;
Best Local Similarity 25.2%; Pred. No. 4e-12;
Matches 56; Conservative 45; Mismatches 108; Indels 13; Gaps 6;
QY 50 IASFIHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLVNYMD 109
DB 28 LRAMLKAEETCAPSVSYFKVCYQEVYL-PSMRKIVATWMLEVCEQKCEEEVFPLAMNYLD 86
QY 110 RFLDSRRLEPTNGWPLQLVSVACLSLAKMEE--PLVPSLDDQIEGAKYIFEPRTIRRM 167
DB 87 RFLSLPEVAKSR--LQLLGATCFEVAASKMKETIPLTAEKLCITYDGS--IRPEELIQM 140
QY 168 ELLVLGVLDWRLRSVTPPLCFLAFFACKVDSTGTFRFLISRATEIIVSNIQEASFLAWP 227
DB 141 ELLLVNKLWNLAAMTPHDFIEHFLSKMPEAEENKQIRKHAQTFVALCATDVKFTISNPP 200
QY 228 SCIAAAAILTAANEIPNWSVVKPENAESWCEGLR-KEKVIQC 268
DB 201 SMVAAGSYVAA---VKGLNLRSPNNFLSYRRLTRFLSRVTKC 239

RESULT 9
US-08-464-517-4
Sequence 4, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mathew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-517-4

Query Match 10.1%; Score 177.5; DB 2; Length 309;
Best Local Similarity 25.6%; Pred. No. 4.3e-12;
Matches 69; Conservative 43; Mismatches 139; Indels 19; Gaps 8;
QY 39 PPSPTTE-DCYSIASFIHERNFVPGFEYLSRFQSRSLDANAREESVGWILKVHAYYGFQ 97
DB 36 PPGAMELLCHEYDP-VRREERYLPQCSYFKCVQ-KDIQPYMRWVATWMLEVCEQKCE 93
QY 98 PLTAYLVANNYMDRFLDSRRLEPTNGWPLQLVSVACLSLAKMEE--PLVPSLDDQIEGA 155
DB 94 EEVPLAMNYLDRFLAGVPTPKSH--LQLLGAVCMFLASKLETSPLTAEKLCITYDNS 150
QY 156 KYIFEPRTIRRMELVLGVLDWRLRSVTPPLCFLAFFACKVDSTGTFRFLISRATEIIVS 215
DB 151 ---IKPQELLEWEVLVGLKLNLAAYTPHDFIEHLRKLPQOREKLSLRKHAQTFIAL 207
QY 216 NIOEASFLAYWPCIAAAAILTAANEIPNWSVVKPENAESWCEGLR--EKVIGCYQLMQ 273
DB 208 CATDFKAMYPSPMIATGSGVAICGLQDEEVSSLTCDALTELLAKITNTDVCCLKACQ 267
QY 274 ELVINNNQRKLPPLKVLPLQLRVTRTRMRS 303
DB 268 D-----QIEAVLNLSLQYRQDQRDGSKS 291

RESULT 10
US-08-463-772-4
Sequence 4, Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

```

: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII(text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/463,772
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/963,308
: FILING DATE: 16-OCT-1992
: APPLICATION NUMBER: US 07/888,178
: FILING DATE: 26-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,514
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Matthew P. Vincent
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MI-004C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 309 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-08-463-772-4

```

Query Match	10.1%;	Score 177.5;	DB 3;	Length 309;
Best Local Similarity	25.6%;	Pred. No. 4.3e-12;		
Matches 69;	Conservative 43;	Mismatches 139;	Indels 19;	Gaps 8;

```
OY      39 PPSPTE-DCYSIASFIEHERNEVPGEFLSRFOQRSLDANARESVGILKVHAYYGQ    97  
        ||   | : : : | : : | : : | : : |  
Db     36 PPGLAMELLCHEVDP-VRREERYLPQCSTFKCVQ-KDIOPYMRMYATWMLEVCCEOKCE  93  
  
OY      98 PLTAYLAVNYMDRFELDSRRLLPETNGWPLOLYSVACLSLAAKME--PLVPSLLDLQIEGA  155  
        ||:|||:||| :::||| |:||||| || : :::  
Db     94 EEVEFLAMNYYLDRELAGVPTPKSH--LQLLGAVCMFLASKLETSPLEKLCITYDNS    150  
  
OY     156 KYIPEPTRIRRMELLVLGLDWRLRSYTPCLCFIAFFACKVDSTGTIFIRELISRATEIIYS  215  
        :||: | :|:| | | | :||| |: : : : : :  
Db     151 ---IKPOELLEWEMLVVGKLKKWNLAAYPHDFEIHILRKLPQOREKLSLRKHQAOTIAL  207  
  
OY     216 NIOEASFAYWPSCTAAAILTTAANEIPMWSVKPENAESWCEDLRK--EKVICGYOLMQ    273  
        : | | | | | : : | : : : : | : : : : :  
Db     208 CATDEKFAMYPPSMITATGSVGAICGLQODEEVSSLTCDALTELAKITTNTDVCLKACQ    267  
  
OY     274 ELVINNNORKLPLELVLPOLRVTTTRIMRS    303  
        : : | : | | | | | : : : : : : : : : :  
Db     268 D-----QIEAVLINSLQOYRQODRGSGS    291
```

RESULT 11

US-08-246-361A-4

; Sequence 4, Application US/08246361A

Patent No. 5998582

; GENERAL INFORMATION:

APPLICANT: BEACH, David H.

TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

NUMBER OF SEQUENCES: 50 ;

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COC

STREET: 60 State Street

CITY: Boston

STATE: MA ;

COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

;
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```

1  OPERATING SYSTEM:  PC-DOS/MS-DOS
2  SOFTWARE:  ASCII(text)
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER:  US/08/246,361A
5  FILING DATE:  19-MAY-1994
6  CLASSIFICATION:  435
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER:  US 07/963,308
9  FILING DATE:  16-OCT-1992
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER:  US 07/888,178
12 FILING DATE:  26-MAY-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER:  US 07/701,514
15 FILING DATE:  16-MAY-1991
16 ATTORNEY/AGENT INFORMATION:
17 NAME:  Matthew P. Vincent
18 REGISTRATION NUMBER:  36,709
19 REFERENCE/DOCKET NUMBER:  MIT-004C
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE:  (617) 227-7400
22 TELEFAX:  (617) 227-5941
23 INFORMATION FOR SEQ ID NO:  4:
24 SEQUENCE CHARACTERISTICS:
25     LENGTH:  289 amino acids
26     TYPE:  amino acid
27     TOPOLOGY:  linear
28     MOLECULE TYPE:  protein
29
30 US-08-246-361A-4

```

Query Match	10.0%;	Score 176.5;	DB 2;	Length 289;
Best Local Similarity	26.3%;	Pred. No. 5e-12;		
Matches 66;	Conservative 39;	Mismatches 129;	Indels 17;	Gaps 6;

```
QY      57 ERNFVPGFEYLSTRFQSRLDANARESVGWILKVHAYYGOPPLTAYLAVNYMDRFLDSRR   116
        |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db     34 EERYLPQCSTFKCYQ-KDIQPRMKNVAITWMLVECEEOKCEEEVFPLAMNYLDRELAGVP   92

QY     117 LPETNGWPLOLVSAACLSLAAKMEE--PLVPSLBDLOIEGAKYIFEPRTIRRMELVLGV   174
        |::: |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db      93 TPKSH--LQLGAVCMFLASKLKETSBLTAEKLCITYTDNS---IKPOLLEWEELVVLGK   146

QY     175 LDWRLRSVTPCLCFLAFFACKVDSTGTFTREFLISRATEIIVSNIQEASFLAYWPSCIAAAA   234
        | | | :||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db     147 LKWNLAAVTPHDFTEHLIRKLPOQREKSLIRKHAQTIALCATDEKFAMYPPSMATGS    206

QY     235 ILTANEIPNWSVVKPENAESWCGLRK--EKVIGCYQLMQELVINNNQRKLPILKVLBPQ   292
        | | | : |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db     207 VGAAICGLQODEEVSSLTCDAITELLAKITNTDVDCCLKACE-----QIEAVLNLSLQQ   260

QY     293 LRVTTRTRMRSS    303

Db     261 YRQDQRDGSKS    271
```

RESULT 12

PCT-US93-05000-4

; Sequence 4, Application PC/TUS9305000

; GENERAL INFORMATION:

APPLICANT: MITOTIX

TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Broo

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

; COUNTRY: US

; ZIP: 02173

; COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

```

;
OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-4

```

Query Match	10.0%;	Score 176.5;	DB 5;	Length 289;
Best Local Similarity	26.3%;	Pred. NO. 5e-12;		
Matches 66;	Conservative 39;	Mismatches 129;	Indels 17;	Gaps 6;

[illegible]

```

RESULT 13
US-08-770-761A-5
; Sequence 5, Application US/08770761A
; Patent No. 5814503
;
GENERAL INFORMATION:
;
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A

```

```

? FILING DATE: 19-DEC-1996
?
? CLASSIFICATION: 530
?
? ATTORNEY/AGENT INFORMATION:
?
? NAME: Gaylo, Paul J.
?
? REGISTRATION NUMBER: 36,808
?
? REFERENCE/DOCKET NUMBER: X-10136
?
? TELECOMMUNICATION INFORMATION:
?
? TELEPHONE: 317-376-0756
?
? TELEFAX: 317-277-1917
?
? INFORMATION FOR SEQ ID NO: 5:
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 662 amino acids
?
? TYPE: amino acid
?
? STRANDEDNESS: single
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: peptide
?
US-08-770-761A-5

```

Query Match	9.98;	Score 173.5;	DB 2;	Length 662;
Best Local Similarity	23.7%;	Pred. No. 4.4e-11;		
Matches 63;	Conservative 52;	Mismatches 136;	Indels 15;	Gaps 7;

```

QY 6 LSDYDLJCGEBSGILSGESPECSFSDIDSSPPPPSPPTTEDCYSIASFIEHERNFVPGEE 65
    : : | | | | | : : | : : | : : : : : |
Db 18 ISEEDLLVPRGSLLAHERQLCCCEVETIRRAYPDANLLNDRV--LRAMLKAEETCAPSVS 75

QY 66 YLSRFQSRSLDANAREESVGWILKVHAYYGFQPLTAYLAVNYMDRFLDSRRLPETNGWPL 125
    | | | | | : : | : : | : : | : : | : : | : : |
Db 76 YFKCVQKEVL-PSMRKIVATWMLLEVCEBQKCEEVFPPLAMNYLDRELSLEPVKKSR--L 131

QY 126 QLVSVACLISLAKMEE--PLVP SILDIQIEGAKYIFEPRTIRRMELLVLGLDWRLRSVT 183
    | | : : : | : | | | : : : : : | : : | : : | : : |
Db 132 QLIGATCMFVASKMKETIPLTAEKLCIYTDNS--IRPELLQMELLLVNKLKWNLAAMT 188

QY 184 PLCLAFACAKVDYSTGTFI RFLISRATETIVSNIQEASFVAYWPSCIAAAAILTAANEIP 243
    | | : : | : : : : | : : : : : | : : | : : | : : |
Db 189 PHDFIEHFLSKMPEAEENKQIRKHAQTFVALCATDVKFISNPPSMAAGSVAA---VQ 245

QY 244 NMSVVKPENAESWCEGLR-KEKVI GC 268
    : : | | | : : | : : | : : | : : | : : |
Db 246 GLNLRSPNNFLSYRRLTRFLSRVIKC 271

```

RESULT 14
US-08-770-761A-7

;; Sequence 7, Application US/08770761A
; Patent No. 5814503

; GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kovacevic, Steven
 ADDRESS: 0440 1014th A

APPLICANT: PAC Ramachandra N

APPLICANT: Rao, Ramachandra N.

TITLE OF INVENTION: FUSION PROTEINS COM

TITLE OF INVENTION: REGULATORY PROTEINS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: P.O. Box 6000

STREET: Lilly Corporate Center/Patent Division

CITY: Indianapolis

STATE: IN

COUNTRY: USA

ZIP: 46285

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/0

FILING DATE: 19-DEC-2011
CLASSIFYING OFFICE: E30

CLASSIFICATION: 330

NAME: Gavlio, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-770-761A-7

Query Match 9.8%; Score 173.5; DB 2; Length 705;
Best Local Similarity 23.7%; Pred. No. 4.8e-11;
Matches 63; Conservative 52; Mismatches 136; Indels 15; Gaps 7;

QY 6 LSDYDLGCGEDSSGILSGSPSCSPSDIDSSPPPTPTEDCYSIASFIEHERNFVPGFE 65
DB 32 ISEEDLVPRGSLAMEHQICCEVETIRRAYPDANLNDV--LRAMIKAEETCAPSVS 89
QY 66 YLSRQSRSLDANAREESVWILKVHAYYGFQPLTAYLVNMDRFLDSRRLPETNGWPL 125
DB 90 YFKCVQKEVL-PSMRKIIVATWMLLEVCEQKCEEEVPLAMNYLDRFLSLEPVKKSR--L 145
QY 126 QLVSVACISLAAMEE--PLVPSLLDLQIEGAKYIFEPRTIRRMELVLGVLDWRLRSVT 183
DB 146 QLLGATCMFVASKMKETIPLTAEKLCITYDNS--IRPELLQMLLVNKLKWLAAAMT 202
QY 184 PLCFIAFACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYWPSCIAAAAILTAAANEIP 243
DB 203 PHDFIEHFLSKMPEAEENKQIRKHAQTFVALCATDVKFKISNPPSMAAGSVVAA--VQ 259
QY 244 NMSVVKPENAESWCGLR-KEKVIGC 268
DB 260 GLNLRSPPNNFLSYRLTRFLSRVVKC 285

RESULT 15

US-07-947-120-8
Sequence 8, Application US/07947120
Patent No. 5538846

GENERAL INFORMATION:

APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and Assay Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/947,120
FILING DATE: 19920917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-947-120-8

Query Match 9.8%; Score 171.5; DB 1; Length 295;
Best Local Similarity 24.8%; Pred. No. 2e-11;
Matches 55; Conservative 45; Mismatches 109; Indels 13; Gaps 6;

QY 50 IASFIHERNFVPGFEYLSRFSRLDANAREESVWILKVHAYYGFQPLTAYLVNMD 109
DB 28 LRAMIKAEETCAPSVSYFKCVQKEVL-PSMRKIIVATWMLLEVCEQKCEEEVPLAMNYLD 86
QY 110 RFLDSRRLPETNGWPIQIVSVACISLAAMEE--PLVPSLLDLQIEGAKYIFEPRTIRRM 167
DB 87 RFLSLEPVKKSR--LQILGATCMFVASKMKETIPLTAEKLCITYDNS--IRPELLQML 140
QY 168 ELVLGVLDWRLRSVTPICFLAFACKVDSTGTFFIRFLISRATEIIVSNIQEASFLAYWP 227
DB 141 ELLVYNKLKWLAAAMTPHDFIEHFLSKMPEAEENKQIRKHAQTFVALCATDVKFKISNPP 200
QY 228 SCIAAAAILTAAANEIPNMSVVKPENAESWCGLR-KEKVIGC 268
DB 201 SVAAGSVVAA--VQGLNLRSPPNNFLSYRLTRFLSRVVKC 239

Search completed: October 23, 2002, 14:39:51
Job time : 14 secs